

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:42:12 ; Search time 60.37 Seconds
(without alignments)
15.917 Million cell updates/sec

Title: US-09-165-546A-7

Perfect score: 57

Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	75.4	274	2 B84930	H+-transporting ATP
2	38	66.7	65	2 S38469	hypothetical prote
3	38	66.7	408	2 C82178	conserved hypothet
4	38	66.7	478	2 T25899	hypothetical prote
5	38	66.7	996	2 F86410	protein F3M18.12
6	37	64.9	113	2 I38320	T-cell receptor be
7	37	64.9	196	2 AE2876	conserved hypothet
8	37	64.9	198	2 G97652	hypothetical prote
9	37	64.9	365	1 B64228	hypothetical prote
10	36	63.2	137	2 D58723	hypothetical prote
11	36	63.2	193	2 F65090	hypothetical 15.2
12	36	63.2	193	2 F85963	hypothetical prote
13	36	63.2	193	2 G91118	hypothetical prote
14	36	63.2	193	2 AF0889	conserved hypothet
15	36	63.2	288	2 G90368	hypothetical prote
16	36	63.2	383	2 JC2472	brain and reproduc
17	36	63.2	1054	2 S54473	TPS3 protein - yea
18	36	63.2	1070	2 S46755	hypothetical prote
19	35.5	62.3	83	1 W5WLHS	E5 protein - human
20	35	61.4	142	2 C82728	succinate dehydrog
21	35	61.4	224	2 G96527	protein F2J15.18
22	35	61.4	270	2 A34636	Fc-gamma receptor
23	35	61.4	299	2 S73406	hypothetical prote
24	35	61.4	316	2 S50336	NADH dehydrogenase
25	35	61.4	380	2 A83458	hypothetical prote
26	35	61.4	483	2 T03909	hypothetical prote
27	35	61.4	492	2 S74338	glycolate oxidase
28	35	61.4	577	2 T09024	proline-rich prote
29	35	61.4	612	2 T39684	hypothetical prote

30	35	61.4	974	2 A86263	Fl3K23.18 protein
31	35	61.4	1950	2 S12332	ubiquitin--protein
32	35	61.4	2103	1 JQ1621	genome polypeptide
33	34	59.6	80	2 AB0913	conserved hypothet
34	34	59.6	132	1 RWMS12	T-cell receptor ga
35	34	59.6	135	1 RWMSV1	T-cell receptor ga
36	34	59.6	137	2 E26420	T-cell receptor ga
37	34	59.6	138	2 G27639	T-cell receptor ga
38	34	59.6	138	2 A27639	T-cell receptor ga
39	34	59.6	138	2 D27639	T-cell receptor ga
40	34	59.6	139	2 F27639	T-cell receptor ga
41	34	59.6	139	2 B27639	T-cell receptor ga
42	34	59.6	139	2 C27639	T-cell receptor ga
43	34	59.6	139	2 E27639	T-cell receptor ga
44	34	59.6	156	2 AH1363	hypothetical prote
45	34	59.6	206	2 T25139	hypothetical prote

ALIGNMENTS

RESULT 1

B84930

H+-transporting ATP synthase (EC 3.6.1.34) A chain [Imported] - Buchnera sp. (strain C:Species: Buchnera sp.)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug-2001

C:Accession: B84930

R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.

A:Reference number: B84930; MUID:20445173

A:Accession: B84930

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-274 <STO>

A:Cross-references: GB:AP000398; GSPDB:GN00144

A:Experimental source: strain APS

C:Genetics:

A:Gene: atpB; BU002

C:Superfamily: H+-transporting ATP synthase protein 6

C:Keywords: hydrolase

Query Match 75.4%; Score 43; DB 2; Length 274;
Best Local Similarity 80.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10

||| |||||

Db 229 LLPWWTQCFL 238

RESULT 2

S38469

hypothetical protein D65 - Desulfohalococcus mobilis (fragment)

C:Species: Desulfohalococcus mobilis

C:Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jul-2000

C:Accession: S38469; S38469

R:Ceccarelli, E.; Bocchetta, M.; Creti, R.; Sanangelantonio, A.M.; Tiboni, O.; Cammarara

Mol. Gen. Genet. 246, 687-696, 1995

A:Title: Chromosomal organization and nucleotide sequence of the genes for elongation

obillis.

A:Reference number: S54733; MUID:95206243

A:Accession: S54733

A>Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-65 <CE2>

A:Cross-references: EMBL:X73582; NID:g410438; PIDN:CAA51989.1; PID:g410444

Query Match

Best Local Similarity 66.7%; Score 38; DB 2; Length 65;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLMWITQCF 10
 Db 6 LTMWYARCF 15

RESULT 3
 C82178
 conserved hypothetical protein VC1609 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: C82178
 R:Heidelbergl, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Esmolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. L. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833
 A:Accession: C82178
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-408 <HEI>
 A:Cross-references: GB:AE004239; GB:AE003852; NID:g9656130; PIDN:AAF94763.1; GSPDB:GN0011
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC1609
 A:Map position: 1

Query Match 66.7%; Score 38; DB 2; Length 408;
 Best Local Similarity 62.5%; Pred. No. 32;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLMWITQCF 9
 Db 345 LWLWACF 352

RESULT 4
 T25899
 hypothetical protein T20F7.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T25899
 R:Miller, N.; Gattung, S.
 submitted to the EMBL Data Library, April 1997
 A:Description: The sequence of C. elegans cosmid T20F7.
 A:Reference number: Z20107
 A:Accession: T25899
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-478 <MIL>
 A:Cross-references: EMBL:U97550; PIDN:AA852856.1; GSPDB:GN000028; CESP:T20F7.6
 A:Experimental source: strain Bristol N2; clone T20F7
 C:Genetics:
 A:Gene: CESP:T20F7.6
 A:Map position: X
 A:Introns: 33/3; 112/2; 144/1; 205/3; 263/2; 300/3; 380/3; 402/2; 451/1

Query Match 66.7%; Score 38; DB 2; Length 478;
 Best Local Similarity 62.5%; Pred. No. 36;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLMWITQCF 9
 Db 43 LLWINQCY 50

RESULT 5
 F86410
 protein F3M18.12 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: F86410
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Lin, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzella Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talbot, K. M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719
 A:Accession: F86410
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-996 <STO>
 A:Cross-references: GB:AE005172; NID:g6560764; PIDN:AAF16764.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F3M18.12
 A:Map position: 1

Query Match 66.7%; Score 38; DB 2; Length 996;
 Best Local Similarity 55.6%; Pred. No. 69;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLMWITQCF 10
 Db 209 VWWLTCFL 217

RESULT 6
 I38320
 T-cell receptor beta chain V region (V-beta 26, germline) precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000
 C:Accession: I38320
 R:Sligham, J.L.; Siemieniak, D.R.; Sieu, L.C.; Koop, B.F.; Hood, L.
 Genomics 20, 149-168, 1994
 A:Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor
 A:Reference number: A54302; MUID:94292194
 A:Accession: I38320
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-113 <RES>
 A:Cross-references: EMBL:U03115; NID:g467918; PIDN:AAA17719.1; PID:g467929
 C:Genetics:
 A:Gene: TCRBV26S1
 A:Introns: 17/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: T-cell receptor
 F:35-113/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 37; DB 2; Length 113;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLMWITQCF 10
 Db 5 LLCWVTLCLL 14

RESULT 7
 AE2876
 conserved hypothetical protein Atu2439 [imported] - Agrobacterium tumefaciens (strain C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C:Accession: AE2876
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woorage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.

A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AF2876

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-196 <KUR>

A:Cross-references: GB:AF008688; PIDN:AAL43427.1; PID:g17740928; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu2439

A:Map position: circular chromosome

Query Match 64.9%; Score 37; DB 2; Length 196;

Best Local Similarity 66.7%; Pred. No. 25;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLMWITOCF 9

|||||

Db 24 LLMWVTPAF 32

RESULT 8

G97652

hypothetical protein AGR_C_4424 [imported] - *Agrobacterium tumefaciens* (strain C58, Cere

C:Species: *Agrobacterium tumefaciens*

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002

C:Accession: G97652

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,

A.: Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*

A:Reference number: A97359; PMID:11743194

A:Accession: G97652

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-198 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK88176.1; PID:gl5157620; GSPDB:GN00169

C:Genetics:

A:Gene: AGR_C_4424

A:Map position: circular chromosome

Query Match

Best Local Similarity 64.9%; Score 37; DB 2; Length 198;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLMWITOCF 9

|||||

Db 26 LLMWVTPAF 34

RESULT 9

B64228

hypothetical protein MG255 - *Mycoplasma genitalium*

C:Species: *Mycoplasma genitalium*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999

C:Accession: B64228

M.: Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;

M.: Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.;

C.A.; Venter, J.C.

Science 270, 397-403, 1995

A:Title: The minimal gene complement of *Mycoplasma genitalium*.

A:Reference number: A64200; MUID:96026346

A:Accession: B64228

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-365 <TIGR>

A:Cross-references: GB:U39703; GB:L43967; NID:gl045933; PID:gl045946; TIGR:MG255

A:Experimental source: strain G-37

C:Genetics:

A:Genetic code: SGC3

C:Superfamily: Mycoplasma hypothetical protein MG255

Query Match

Best Local Similarity 64.9%; Score 37; DB 1; Length 365;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LLMWITOCFL 10

|||||

Db 117 LLMWROCWL 125

RESULT 10

D58723

hypothetical protein (orf4, cpdA 5' region) - *Escherichia coli*

C:Species: *Escherichia coli*

C:Date: 18-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Feb-1998

C:Accession: D58723

R:Imamura, R.; Yamanaka, K.; Ogura, T.; Hiraga, S.; Fujita, N.; Ishihama, A.; Niki, F.

J. Biol. Chem. 271, 25423-25429, 1996

A:Title: Identification of the cpdA gene encoding cyclic 3',5'-adenosine monophosphate

A:Reference number: A58723; MUID:96411758

A:Accession: D58723

A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-137 <IMA>

A:Cross-references: GB:D16557; NID:9453393

A:Experimental source: strain K-12

C:Genetics:

A:Map position: 68.4 min

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 137;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WITOCFL 10

|||||

Db 77 WLSQCFM 83

RESULT 11

E65090

hypothetical 15.2 kD protein in *icc* 3' region - *Escherichia coli* (strain K-12)

C:Species: *Escherichia coli*

C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999

C:Accession: E65090

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.: Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: E65090

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-193 <BLAT>

A:Cross-references: GB:AE000385; GB:U00096; NID:gl789405; PIDN:AAC76067.1; PID:gl7894

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: yqiA

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 193;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WITOCFL 10

|||||

Db 77 WLSQCFM 83

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RESULT 12
F85963
hypothetical protein yqiA [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: F85963
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.;
Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85963
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <STO>
A:Cross-References: GB:AE005174; NID:g12517609; PIDN:AAG58170.1; GSPDB:GN00145; UWGP:243
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yqiA

Query Match 63.2%; Score 36; DB 2; Length 193;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WITQCFL 10
Db 77 WLSQCFM 83

RESULT 13
G91118
hypothetical protein ECS3919 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: G91118
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G91118
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <HAY>
A:Cross-References: GB:BA000007; PIDN:BAB37342.1; PID:g13363392; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECS3919

Query Match 63.2%; Score 36; DB 2; Length 193;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WITQCFL 10
Db 77 WLSQCFM 83

RESULT 14
AF0889
conserved hypothetical protein STY3360 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AF0889
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

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A:Reference number: AB0502; PMID:11677608
A:Accession: AF0889
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <PAR>
A:Cross-References: GB:AL513382; PIDN:CAD03014.1; PID:g16504259; GSPDB:GN00176
C:Genetics:
A:Gene: STY3360

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Query Match 63.2%; Score 36; DB 2; Length 193;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 4 WITQCFL 10
Db 77 WLSQCFM 83

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RESULT 15
G90368
hypothetical protein acaA-4 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: G90368
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch.;
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: G90368
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <KUR>
A:Cross-References: GB:AE006641; NID:g13815300; PIDN:AAK42206.1; GSPDB:GN00155
C:Genetics:
A:Gene: acaA-4

```

```

Query Match 63.2%; Score 36; DB 2; Length 288;
Best Local Similarity 55.6%; Pred. No. 52;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 2 LMWITQCFL 10
Db 280 LLYITQCYM 288

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Search completed: July 16, 2002, 07:48:18
Job time: 366 sec

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SEARCH REQUEST FORM

Scientific and Technical Information Center

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Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

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 jan.delaval@uspto.gov

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Searcher: <u>Jan Delaval</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>703-308-4498</u>	AA Sequence (#) <u>✓</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>7/16/02</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>7/16/02</u>	Litigation _____	Lexis/Nexis <u>✓</u>
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
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Online Time: <u>10</u>	Other _____	Other (specify) _____

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Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Type of Search

NA Sequence (#) _____
 AA Sequence (#) _____
 Structure (#) _____
 Bibliographic _____
 Litigation _____
 Fulltext _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

STN _____
 Dialog _____
 Questel/Orbit _____
 Dr.Link _____
 Lexis/Nexis _____
 Sequence Systems _____
 WWW/Internet _____
 Other (specify) _____

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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:47:02 ; Search time 32.19 Seconds
(without alignments)
12.028 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFLL 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	57	100.0	180	1 CTAG_HUMAN	P78358 homo sapien
2	43	75.4	274	1 ATP6_BUCAI	P57118 buchnera ap
3	37	64.9	365	1 Y255_MYCGE	P47497 mycoplasma
4	36	63.2	193	1 YQIA_ECOLI	P36653 escherichia
5	36	63.2	351	1 V0D1_ARATH	Q91J15 arabidopsis
6	36	63.2	351	1 V0D2_ARATH	Q91H44 arabidopsis
7	36	63.2	1022	1 TPS3_YEAST	P38426 saccharomyc
8	36	63.2	1070	1 YHV4_YEAST	P38850 saccharomyc
9	35.5	62.3	83	1 VE5_HPV16	P06927 human papil
10	35	61.4	299	1 Y0G0_MYCPN	P75042 mycoplasma
11	35	61.4	341	1 FCG2_CAVPO	Q60513 cavia porce
12	35	61.4	1950	1 UBRI_YEAST	P19812 saccharomyc
13	35	61.4	2103	1 RRPL_UUK	P33433 ukunilemi v
14	34	59.6	132	1 TVC3_MOUSE	P06324 mus musculu
15	34	59.6	135	1 TVC1_MOUSE	P01740 mus musculu
16	34	59.6	219	1 DCK1_FOWPV	P21974 fowlpox vir
17	34	59.6	353	1 YRRI_BACSU	Q34472 bacillus su
18	34	59.6	385	1 YEHY_ECOLI	P33361 escherichia
19	34	59.6	495	1 ACHP_RAT	P12392 rattus norv
20	34	59.6	504	1 PSD3_CABEL	Q04908 caenorhabdi
21	34	59.6	1502	1 MRP6_RAT	Q08269 rattus norv
22	34	59.6	1503	1 MRP6_HUMAN	Q95255 homo sapien
23	34	59.6	2670	1 IP3T_RAT	P06329 rattus norv
24	34	59.6	2671	1 IP3T_HUMAN	Q14573 homo sapien
25	33	57.9	114	1 APR2_HUMAN	Q9y5m1 homo sapien
26	33	57.9	215	1 CIB3_HUMAN	Q9ny72 homo sapien
27	33	57.9	255	1 FOLI_MOUSE	P35846 mus musculu
28	33	57.9	276	1 HEMX_BACSU	P16645 bacillus su
29	33	57.9	345	1 C5AR_CAVPO	Q70129 cavia porce
30	33	57.9	375	1 AMSC_ERWAM	Q46633 erwinia amy
31	33	57.9	465	1 LIPP_CAVPO	P50903 cavia porce
32	33	57.9	498	1 ACHP_HUMAN	P30926 homo sapien
33	33	57.9	603	1 NMBL_MOUSE	Q08919 mus musculu

34 33 57.9 609 1 NMBL_HUMAN Q9y6r0 homo sapien
35 33 57.9 811 1 RFXL_YEAST P48743 saccharomyc
36 33 57.9 972 1 CSEL_ARATH Q9zpv7 arabidopsis
37 33 57.9 1054 1 HMD1_YEAST P12683 saccharomyc
38 33 57.9 1179 1 VGS6_HSV11 Q00099 ictalurid h
39 33 57.9 2124 1 Y192_HUMAN Q93074 homo sapien
40 33 57.9 3110 1 HD_RAT P51111 rattus norv
41 33 57.9 3119 1 HD_MOUSE P42859 mus musculu
42 32.5 57.0 250 1 TIFC_ORYSA P50156 oryza sativ
43 32 56.1 85 1 YD44_HSVSC P22578 herpesvirus
44 32 56.1 163 1 PHZA_PSEFL Q51787 pseudomonas
45 32 56.1 217 1 FDN1_ECOLI P24185 escherichia

ALIGNMENTS

RESULT 1
CTAG_HUMAN ID CTAG_HUMAN STANDARD; PRT; 180 AA.
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Autoimmunogenic cancer/testis antigen NY-ESO-1.
GN CTAG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97203161; PubMed=9050879;
RA Chen Y.-T., Scantlan M.J., Sahin U., Tuerci O., Gure A.O., Tsang S.,
RA Williamson B., Stockert E., Pfleundschuh M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected
by autologous antibody screening.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1 a new gene with tumor specificity.";
RL Inc. J. Cancer 76:903-908(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98430682; PubMed=9759882;
RA Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA Schwartzentruber D.J., Rosenberg S.A.;
RT "A breast and melanoma-shared tumor antigen: T cell responses to
antigenic peptides translated from different open reading frames.";
RL J. Immunol. 161:3596-3606(1998).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND OVARY AND IN A WIDE
VARIETY OF CANCERS. DETECTED IN UTERINE MYOMETRIUM.
CC -!- SIMILARITY: STRONG, TO LAGE-1.
CC
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CC
CC EMBL: U87459; AAB49693.1;
CC EMBL: AF003149; CAA05908.1;
CC EMBL: AF038567; AAD05202.1;
CC MIM: 300156;
CC
CC DOMAIN 5 82 GLY-RICH.
CC TRANSMEM 156 172 POTENTIAL.

SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 57; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
||| |
Db 158 LLMWITQCFL 167

RESULT 2
ATP6_BUCAI STANDARD; PRT; 274 AA.

AC P57118;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP synthase A chain (EC 3.6.3.14) (Protein 6).

GN ATPB OR B0002.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;

RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. APS.";

RL Nature 407:81-86(2000).
CC -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE
 (BY SIMILARITY).

CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
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 or send an email to license@isb-sib.ch).

CC -----
DR EMBL; AP001118; BAB12730.1; -;
DR InterPro; IPR000568; ATP_synt_A.
DR Pfam; PF00119; ATP_synt_A; 1.
DR PRINTS; PR00123; ATPASEA.
DR PROSITE; PS00449; ATPASEA; 1.

KW Hydrogen ion transport; CF(0); Transmembrane; Complete proteome.
FT TRANSMEM 44 64.
FT TRANSMEM 110 130 POTENTIAL.
FT TRANSMEM 156 176 POTENTIAL.
FT TRANSMEM 179 199 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
SQ SEQUENCE 274 AA; 31363 MW; 4B2321336EFE78A4 CRC64;

Query Match 75.4%; Score 43; DB 1; Length 274;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
||| |
Db 229 LLMWITQCFL 238

RESULT 3
Y255_MYCGE STANDARD; PRT; 365 AA.
ID P47497; Q49289; Q49297;
AC 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG255.
GN MG255.

OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 Fritschmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
 Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 Tomb J.-F., Dougherty B.A., Bitt K.F., Hu P.-C., Lucier T.S.,
 Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

RL "The minimal gene complement of Mycoplasma genitalium.";
 Science 270:397-403(1995).
RN [2]

RP SEQUENCE OF 134-365 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;

RA Peterson S.N., Hu P.-C., Bitt K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
 sequencing.";

RL J. Bacteriol. 175:7918-7930(1993).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----

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CC -----
DR EMBL; U39704; AAC71475.1; -;
DR EMBL; U02174; RAD12457.1; -;
DR EMBL; U02164; RAD12446.1; -;
DR TIGR; MG255; -;
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 151 171 POTENTIAL.
FT TRANSMEM 187 207 POTENTIAL.
FT CONFLICT 180 180 N -> KR (IN REF. 2).

SQ SEQUENCE 365 AA; 42440 MW; 6609C2C8CA2CC5B7 CRC64;

Query Match 64.9%; Score 37; DB 1; Length 365;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLMWITQCFL 10
||| |
Db 117 LLMWITQCFL 125

RESULT 4
YQ1A_ECOLI STANDARD; PRT; 193 AA.

AC P36653;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein yqia.
GN YQIA OR B3031 OR Z4388 OR ECS3919.
OS Escherichia coli, and
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Ito T.,
RA Ikeda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kudo S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [4]
RP SEQUENCE OF 1-137 FROM N.A.
RC STRAIN=K12;
RA Inamura N., Niki H., Yamanaka K., Ogura T., Fujita N., Ishihama A.,
RA Hiraga S.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; U28377; AAA69199.1; -;
CC EMBL; AE000385; AAC76067.1; -;
CC EMBL; AE005533; AAC58170.1; -;
CC EMBL; AP002564; BAB37342.1; -;
CC EMBL; D16557; -; NOT_ANNOTATED_CDS.
CC EcoGene; EG12186; yqia.
CC InterPro; IPR000379; Est_lip_thioest_actsite.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 135 137 APD -> GRI (IN RFB. 4).
SQ SEQUENCE 193 AA; 21641 MW; 3077DED58BC0E8A3 CRC64;

Query Match 63.28; Score 36; DB 1; Length 193;
Best Local Similarity 57.18; Pred. No. 17;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 4 WITQCF 10
1::111:

Db 77 WLSQCFM 83

RESULT 5
VODL_ARATH
ID VODL_ARATH STANDARD; PRT; 351 AA.
AC Q9LJ15;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable vacuolar ATP synthase subunit d1 (EC 3.6.3.14) (V-ATPase d
subunit 1) (Vacuolar proton pump d subunit 1).
GN AT3G28710 OR MN14.21.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Fartmann B., Vallie G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Schaefer M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D.,
RA Cooke R., Laudie M., Berger-Llauró C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldblum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Ideasa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
RL Nature 408:820-822(2000).
CC -!- FUNCTION: SUBUNIT OF THE INTEGRAL MEMBRANE V0 COMPLEX OF VACUOLAR
CC ATPASE. VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF
CC INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS, THUS PROVIDING
CC MOST OF THE ENERGY REQUIRED FOR TRANSPORT PROCESSES IN THE
CC VACUOLAR SYSTEM.
CC -!- SUBUNIT: V-ATPase is a heteromultimeric enzyme composed of a
CC peripheral catalytic V1 proton pore complex (components A to H) attached to
CC an integral membrane V0 proton pore complex (components: a, c, c',
CC c'', and d).
CC -!- SIMILARITY: BELONGS TO THE V-ATPASE VOD/AC39 SUBUNIT FAMILY.
CC -----
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CC -----
CC EMBL; AP000420; BAB02186.1; -;
CC InterPro; IPR002843; V-ATP-synt_AC39.
CC Pfam; PF01992; V-ATP-synt_AC39; 1.

```
KW Hydrolase; Hydrogen ion transport.
SQ SEQUENCE 351 AA; 40791 MW; 5E1A67A149AC4EF4 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 351;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQC 8
Db 328 LMWISec 334

RESULT 6
VOD2_ARATH
ID VOD2_ARATH STANDARD; PRT; 351 AA.
AC Q9LHA4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable vacuolar ATP synthase subunit d 2 (EC 3.6.3.14) (V-ATPase d
DE subunit 2) (Vacuolar proton pump d subunit 2).
GN ATG328715 OR MN14.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseid M.,
RA Farmanan B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delsen M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quettier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Schaefer M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laude M., Berger-Llauro C., Purnelle B., Masuy D.,
RA De Haan M., Maare A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Waits A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Watanabe A., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana."
RT Nature 408:820-822(2000).
RL Nature 408:820-822(2000).
CC -!- FUNCTION: SUBUNIT OF THE INTEGRAL MEMBRANE V0 COMPLEX OF VACUOLAR
CC ATPASE. VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF
CC INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS. THIS PROVIDING
CC MOST OF THE ENERGY REQUIRED FOR TRANSPORT PROCESSES IN THE
CC VACUOLAR SYSTEM.
CC -!- SUBUNIT: V-ATPase is a heteromultimeric enzyme composed of a
CC peripheral catalytic V1 complex (components A to H) attached to
CC an integral membrane V0 proton pore complex (components: a, c, c',
CC c'', and d).
CC -!- SIMILARITY: BELONGS TO THE V-ATPASE VOD/AC39 SUBUNIT FAMILY.
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```

FT DOMAIN 255 746 TPS COMPLEX DOMAIN.
 FT CONFLICT 154 154 P -> L (IN REF. 1).
 FT CONFLICT 733 733 N -> D (IN REF. 1).
 FT CONFLICT 802 802 S -> G (IN REF. 1).
 FT CONFLICT 870 870 D -> E (IN REF. 1).
 SQ SEQUENCE 1022 AA; 115363 MW; 49AD0A9E194E5962 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 1022;

Best Local Similarity 83.3%; Pred. No. 77;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WITQCF 9

|||||

Db 723 WITKCF 728

RESULT 8

ID YHV4_YEAST STANDARD; PRT; 1070 AA.

AC P38850;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 123.0 kDa protein in SPO16-REC104 intergenic region.

GN YHR154W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RX MEDLINE=94378003; PubMed=8091229;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,

Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,

Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,

Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,

Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,

Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,

Vaudin M.;

"Complete nucleotide sequence of Saccharomyces cerevisiae chromosome

VIII.";

RL Science 265:2077-2082(1994).

CC -1- SIMILARITY: CONTAINS 2 BRCT DOMAINS.

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CC -----

DR EMBL; U10397; AB68978.1; -.

DR PIR; S46755; S46755.

DR SGD; S0001197; ESC4.

DR InterPro; IPR001357; BRCT.

DR SMART; PF00533; BRCT; 5.

DR PROSITE; PS00292; BRCT; 4.

DR PROSITE; PS01172; BRCT; 2.

FW Hypothetical protein; Repeat.

FT DOMAIN 117 210 BRCT 1.

FT DOMAIN 370 466 BRCT 2.

SQ SEQUENCE 1070 AA; 123017 MW; 767931285BB52580 CRC64;

Query Match

Best Local Similarity 63.2%; Score 36; DB 1; Length 1070;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MWITQCF 10

|||||

Db 447 MMLEQCYM 454

RESULT 9

ID VE5_HPV16

AC P06927; STANDARD; PRT; 83 AA.

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Probable E5 protein.

GN E5.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88160059; PubMed=2831662;

RA Bubb V., McCance D.J., Schlegel R.;

"DNA sequence of the HPV-16 E5 ORF and the structural conservation of

its encoded protein.";

RL Virology 163:243-246(1988).

RN [2]

RP SEQUENCE OF 20-83 FROM N.A.

RX MEDLINE=85246220; PubMed=2990099;

RA Seedorf K., Kramer G., Durst M., Suhai S., Rowekamp W.G.;

"Human papillomavirus type 16 DNA sequence.";

RL Virology 145:181-185(1985).

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CC -----

DR EMBL; K02718; AAA46938.1; ALT_SEQ.

DR PIR; A30016; W5WLHS.

DR InterPro; IPR004270; Papilloma_E5.

DR Pfam; PF03025; Papilloma_E5; 1.

KW Early protein.

SQ SEQUENCE 83 AA; 9401 MW; 442COABF0D77CDCF CRC64;

Query Match

Best Local Similarity 62.3%; Score 35.5; DB 1; Length 83;

Matches 7; Conservative 3; Mismatches 0; Indels 5; Gaps 1;

Qy 1 LLMWIT-----QCFL 10

|||||

Db 47 LLLWITAAASAFRCFI 61

RESULT 10

Y060_MYCPN

ID Y060_MYCPN STANDARD; PRT; 299 AA.

AC P75042;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Putative glycosyl transferase MG060 homolog (EC 2.-.-.-)

DE (D09_orf299).

GN MPN075 OR MP080.

OS Mycoplasma pneumoniae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;

OC Mycoplasmataceae; Mycoplasma.

OX NCBI_TaxID=2104;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 29342 / M129;

RX MEDLINE=97105885; PubMed=8948633;

```

RA Himmelreich R., Hilbert H., Plagens H., Pirkil E., Li B.-C.,
RA Hermann R.;
RT "complete sequence analysis of the genome of the bacterium Mycoplasma
RL Nucleic Acids Res. 24:4420-4449(1996)";
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
CC STRONG. TO M.GENITALIUM MG060.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000010; AAB95728.1; -
DR InterPro; IPR001173; Glycosyltransf_2.
DR Pfam; PF00535; Glycosyltransf_2; 1.
KW Hypothetical protein; transferase; Glycosyltransferase;
SQ Complete proteome.
SQ SEQUENCE 299 AA; 35079 MW; 6E3F89EDAE420417 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 299;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 WITOCFL 10
| | | | |
Db 274 WITRCFL 280

RESULT 11
FCG2_CAVPO STANDARD; PRT; 341 AA.
AC Q60513; Q60512; Q60511; Q60498;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Low affinity immunoglobulin gamma FC region receptor II precursor (FC-
gamma RII) (FCRII) (IGG FC receptor II) (FC-gamma-1/gamma-2 receptor).
GN FCGR2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 2R-B1).
RX MEDLINE=90241239; PubMed=1692213;
RA Tominaga M., Sakata A., Ohmura T., Yamashita T., Koyama J., Onoue K.;
RT "The structure and expression of the guinea pig Fc receptor for IgG1
and IgG2 (Fc gamma 1/gamma 2R).";
RL Biochem. Biophys. Res. Commun. 168:683-689(1990).
RN [2]
SEQUENCE FROM N.A. (ISOFORMS 2R-B1; 2R-B2 AND 2R-B3).
RC STRAIN-JY-1;
RX MEDLINE=93346746; PubMed=8345193;
RA Yamashita T., Shinohara K., Yamashita Y.;
RT "Expression cloning of complementary DNA encoding three distinct
isoforms of guinea pig Fc receptor for IgG1 and IgG2.";
RL Immunol. 151:2014-2023(1993).
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS GAMMA. LOW
AFFINITY RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2R-B1, 2R-B2 AND 2R-B3 (SHOWN
HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: MACROPHAGES AND POLYMORPHONUCLEAR LEUKOCYTES
EXPRESS PREFERENTIALLY 2R-B1. B LYMPHOCYTES EXPRESS ALL THREE
FORMS.
CC -!- DOMAIN: CONTAINS AN INTRACITOPLASMIC MOTIF REFERRED AS
IMMUNORECEPTOR TYROSINE-BASED INHIBITOR MOTIF (ITIM). THIS MOTIF
IS INVOLVED IN DOWNMODULATION OF CELLULAR FUNCTIONS.

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CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL; D13693; BAA02852.1; -
DR EMBL; D13692; BAA02851.1; -
DR EMBL; D13691; BAA02850.1; -
DR EMBL; M35272; BAA37036.1; ALT_INIT.
DR HSSP; P12319; IALT.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_Like; 1.
KW Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat; Alternative splicing.
FT SIGNAL 1 42
FT CHAIN 43 341
FT DOMAIN 43 224
FT TRANSMEM 225 245
FT DOMAIN 246 341
FT DOMAIN 64 120
FT DOMAIN 145 203
FT DOMAIN 318 323
FT DISULFID 71 113
FT DISULFID 152 196
FT CARBOHYD 79 79
FT CARBOHYD 106 106
FT CARBOHYD 180 180
FT CARBOHYD 187 187
FT CARBOHYD 195 195
FT VARSPIC 273 301
FT VARSPIC 257 301
FT CONFLICT 114 114
FT SEQUENCE 341 AA; 37091 MW; 5137E3271D443B84 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 341;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMTITOCFL 10
| | | | |
Db 28 MLMTITVFL 37

RESULT 12
UBRL_YEAST STANDARD; PRT; 1950 AA.
AC P19812;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE N-end-recognition protein (Ubiquitin-protein ligase E3 component) (N-
recognition).
GN UBRL OR PTRL OR YGR184C OR G7168.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
SEQUENCE FROM N.A.

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RC STRAIN=S288C / GRF88;
RX MEDLINE=91006011; PubMed=2209542;
RA Bartel B., Wuenning I., Varshavsky A.;
RT "The recognition component of the N-end rule pathway.";
RN EMO J. 9:3179-3189(1990).
RP (2)
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=97279231; PubMed=9133739;
RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M.,
RA Nombela C.;
RT "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm
RT of Saccharomyces cerevisiae chromosome VII.";
RN Yeast 13:357-363(1997).
RP (3)
RP SEQUENCE OF 346-1950 FROM N.A.
RA Hebling U., Hofmann B., Delius H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECOGNITION COMPONENT OF THE N-END RULE PATHWAY. BINDS
CC TO PROTEINS BEARING AMINO-TERMINAL RESIDUES THAT ARE DESTABILIZING
CC ACCORDING TO THE N-END RULE, BUT DOES NOT BIND TO OTHERWISE
CC IDENTICAL PROTEINS BEARING STABILIZING AMINO-TERMINAL RESIDUES.
CC -----
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CC -----
DR EMBL; X53747; CAA37779.1; -.
DR EMBL; X99074; CAA67528.1; -.
DR EMBL; Z72969; CAA97210.1; -.
DR PIR; S12332; S12332.
DR SGD; S0003416; UBRL.
DR InterPro; IPR003126; ZnF_UBRL.
DR InterPro; IPR001841; ZnF_ring.
DR Pfam; PF02207; zf_UBRL; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00396; ZnF_UBRL; 1.
KW Ligase; Ubiquitin conjugation.
SQ SEQUENCE 1950 AA; 224836 MW; 33E4CD3A031AF523 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 1950;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
DB 395 IILWITHC 402
:::|||||
:::|||||

RESULT 13
RRPL_UUK
ID RRPL_UUK STANDARD; PRT; 2103 AA.
AC P33453.
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (L protein).
GN L.
OS Uukuniemi virus (Uuk).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S23;
RX MEDLINE=92333259; PubMed=1629699;
RA Elliott R.M., Dunn E., Simons J.F., Pettersson R.F.;
RT "Nucleotide sequence and coding strategy of the Uukuniemi virus L RNA
RT segment.";

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RL J. Gen. Virol. 73:1745-1752(1992).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC [RNA](N).
CC -----
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CC -----
DR EMBL; D10759; BAA01590.1; -.
DR PIR; JQ1621; JQ1621.
KW Transferase; Nucleotidyltransferase; RNA-directed RNA polymerase.
SQ SEQUENCE 2103 AA; 241039 MW; B0EA708451B0B6BD CRC64;

Query Match 61.4%; Score 35; DB 1; Length 2103;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
DB 1207 LLRWITAC 1214
||| ||| |

RESULT 14
TVC3_MOUSE
ID TVC3_MOUSE STANDARD; PRT; 132 AA.
AC P06324;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE T-cell receptor gamma chain V region DFL12 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85137888; PubMed=3871915;
RA Kranz D.M., Saito H., Heller M., Takagaki Y., Haas W., Eisen H.N.,
RA Toneygawa S.;
RT "Limited diversity of the rearranged T-cell gamma gene.";
RL Nature 313:752-755(1985).
DR PIR; A02019; RWMS12.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW T-cell; Receptor; Signal.
FT SIGNAL 1 18
FT CHAIN 19 132
FT T-CELL RECEPTOR GAMMA CHAIN V REGION
FT DFL12.
FT DOMAIN 19 114
FT DOMAIN 115 132
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 15434 MW; 855D714D04A3CCFE CRC64;

Query Match 59.6%; Score 34; DB 1; Length 132;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
DB 3 LLRWITSCCL 12
||| ||| |

RESULT 15
TVCL_MOUSE

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ID TVCL_MOUSE STANDARD; PRT; 135 AA.
AC P01740;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE T-cell receptor gamma chain V region V108A precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099339; PubMed=3917858;
RA Hayday A.C., Saito H., Gillies S.D., Kranz D.M., Tanigawa G.,
RA Eisen H.N., Tonegawa S.;
RT "Structure, organization, and somatic rearrangement of T cell gamma
RT genes.";
RL Cell 40:259-269(1985).
RN [2]
RP SEQUENCE FROM N.A. (CLONE PHDS4/PHDS203).
RC STRAIN-BALB.B;
RX MEDLINE=84245824; PubMed=6330561;
RA Saito H., Kranz D.M., Takagaki Y., Hayday A.C., Eisen H.N.,
RA Tonegawa S.;
RT "Complete primary structure of a heterodimeric T-cell receptor
RT deduced from cDNA sequences.";
RL Nature 309:757-762(1984).
CC -!- MISCELLANEOUS: THIS MRNA WAS ISOLATED FROM A CYTOTOXIC
CC T-LYMPHOCYTE. THE GENE CORRESPONDING TO THIS MRNA IS REARRANGED
CC SPECIFICALLY IN T CELLS AND ITS ORGANIZATION IS SIMILAR TO AN IG
CC GENE, WITH V (OR V+D), J, AND C REGIONS.
DR PIR; A02018; RWM5V1.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW T-cell; Receptor; Signal.
FT SIGNAL 1 18
FT CHAIN 19 135 T-CELL RECEPTOR GAMMA CHAIN V REGION
FT V108A.
FT DOMAIN 19 116 V SEGMENT.
FT DOMAIN 117 135 J SEGMENT.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15930 MW; 402145C95E924D7D CRC64;

Query Match 59.6%; Score 34; DB 1; Length 135;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
DB 3 LLRWFTSCCL 12

Search completed: July 16, 2002, 08:00:43
Job time: 821 sec
```

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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:45:57 ; Search time 89.54 Seconds
(without alignments)
19,320 Million cell updates/sec

Title: US-09-165-546A-7

Perfect score: 57

Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	57	100.0	180	4	Q9Y479	Q9Y479 homo sapien
2	44	77.2	151	4	Q9UJK3	Q9UJK3 homo sapien
3	44	77.2	593	4	Q96NH3	Q96NH3 homo sapien
4	38	66.7	65	1	Q46517	Q46517 desulfuroco
5	38	66.7	152	12	Q9PX35	Q9PX35 equine arte
6	38	66.7	152	12	Q9PX34	Q9PX34 equine arte
7	38	66.7	152	12	Q9QKH1	Q9QKH1 equine arte
8	38	66.7	152	12	Q9QKH2	Q9QKH2 equine arte
9	38	66.7	152	12	Q9QKH3	Q9QKH3 equine arte
10	38	66.7	273	5	Q962M9	Q962M9 plasmodium
11	38	66.7	408	16	Q9KRW7	Q9KRW7 vibrio chol
12	38	66.7	423	5	O02168	O02168 caenorhabdi
13	38	66.7	996	10	Q9SGP2	Q9SGP2 arabidopsis
14	37.5	65.8	83	12	Q9WGD6	Q9WGD6 human papill
15	37	64.9	317	5	O97336	O97336 plasmodium
16	37	64.9	783	3	O14411	O14411 candida alb

17	37	64.9	1189	5	Q9VQ78	Q9VQ78 drosophila
18	36	63.2	70	12	O90748	O90748 encephalomy
19	36	63.2	71	12	O90751	O90751 encephalomy
20	36	63.2	218	10	Q9LRK4	Q9LRK4 arabidopsis
21	36	63.2	223	10	Q9LRK5	Q9LRK5 arabidopsis
22	36	63.2	255	11	Q9JL02	Q9JL02 rattus norv
23	36	63.2	257	10	Q9LRK3	Q9LRK3 arabidopsis
24	36	63.2	258	10	Q9LRK2	Q9LRK2 arabidopsis
25	36	63.2	288	17	Q97WU4	Q97WU4 sulfolobus
26	36	63.2	298	4	Q9HD97	Q9HD97 homo sapien
27	36	63.2	299	4	Q9UBK4	Q9UBK4 homo sapien
28	36	63.2	299	4	Q9UGN4	Q9UGN4 homo sapien
29	36	63.2	301	4	O95100	O95100 homo sapien
30	36	63.2	311	10	Q9LJW1	Q9LJW1 arabidopsis
31	36	63.2	335	5	Q9XYA7	Q9XYA7 drosophila
32	36	63.2	351	10	Q9FE04	Q9FE04 arabidopsis
33	36	63.2	376	4	Q969X9	Q969X9 homo sapien
34	36	63.2	379	4	Q96F06	Q96F06 homo sapien
35	36	63.2	383	4	Q13880	Q13880 homo sapien
36	36	63.2	415	4	Q9NKR7	Q9NKR7 homo sapien
37	35.5	62.3	70	12	Q9WA26	Q9WA26 human papil
38	35.5	62.3	70	12	Q9W9S8	Q9W9S8 human papil
39	35.5	62.3	70	12	Q9W9F2	Q9W9F2 human papil
40	35.5	62.3	70	12	Q9W8H7	Q9W8H7 human papil
41	35.5	62.3	70	12	Q9W1V2	Q9W1V2 human papil
42	35.5	62.3	70	12	Q9W1V3	Q9W1V3 human papil
43	35.5	62.3	70	12	Q9W1V4	Q9W1V4 human papil
44	35.5	62.3	70	12	Q9W1V6	Q9W1V6 human papil
45	35.5	62.3	70	12	Q9W1V7	Q9W1V7 human papil

ALIGNMENTS

RESULT 1

Q9Y479 PRELIMINARY: PRT; 180 AA.
 ID Q9Y479;
 AC Q9Y479;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE LAGE-1S PROTEIN (CANCER/TESTIS ANTIGEN 2).
 GN LAGE1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MELANOMA;
 RX MEDLINE-99325550; PubMed-10399963;
 RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
 RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
 unexpected translation product of LAGE-1.";
 RL Int. J. Cancer 82:442-448(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
 RA Patlan H., Ciccodicola A., Kenwick S., Platzer M., D'Urso M.,
 RA Nelson D.L.;
 RT "Multiple pathogenic and benign genomic rearrangements occur at a 35-
 kb duplication involving the NEMO and the LAGE2 genes.";
 RL Hum. Mol. Genet. 0:0-0(2001).
 DR EMBL; AJ012834; CAA10194.1; -;
 DR EMBL; AF273315; AAL27015.1; -;
 SQ SEQUENCE 180 AA; 18236 MW; 9077FAP953543A25 CRC64;

Query Match 100.0%; Score 57; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10

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Db 158 LLMWITQCF 167
|||||
RESULT 2
Q9UJK3 PRELIMINARY; PRT; 151 AA.
AC Q9UJK3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DJ310J6.1 (NOVEL PROTEIN) (FRAGMENT).
GN DJ310J6.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Blakey S.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035593; CAB56526.1; -.
FT NON_TER 1
SQ SEQUENCE 151 AA; 17990 MW; 9895001E4CF4B6DE CRC64;

Query Match 77.2%; Score 44; DB 4; Length 151;
Best Local Similarity 87.5%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMWITQCF 9
| | | | |
Db 52 LQWITQCF 59

RESULT 3
Q96NH3 PRELIMINARY; PRT; 593 AA.
AC Q96NH3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CDNA FLJ30899 FIS, CLONE FEBRA2005726.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto K., Isono Y., Kawai-Hio Y., Saico K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murekawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK05461; BAB70925.1; -.
SQ SEQUENCE 593 AA; 68636 MW; B3295013BB2225BC CRC64;

Query Match 77.2%; Score 44; DB 4; Length 593;
Best Local Similarity 87.5%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMWITQCF 9
| | | | |
Db 494 LQWITQCF 501

RESULT 4
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Q46517 PRELIMINARY; PRT; 65 AA.
AC Q46517;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ORFD 65 (FRAGMENT).
OS Desulfurococcus mobilis.
OC Archaea; Crenarchaeota; Desulfurococcaceae; Desulfurococcaceae;
OC Desulfurococcus.
OX NCBI_TaxID=2274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 2126;
RX MEDLINE=95206243; PubMed=7898436;
RA Ceccarelli E., Bocchetta M., Creti R., Sanangelantoni A.M., Tiboni O.,
RA Cammarano P.;
RT "Chromosomal organization and nucleotide sequence of the genes for
RT elongation factors EF-1alpha and EF-2 and ribosomal proteins S7 and
RT S10 of the hyperthermophilic archaeum Desulfurococcus mobilis.";
RL Mol. Gen. Genet. 246:687-696(1995).
DR EMBL; X73582; CAA51989.1; -.
FT NON_TER 65
SQ SEQUENCE 65 AA; 7597 MW; B51DEF4F5C84E0F8 CRC64;

Query Match 66.7%; Score 38; DB 1; Length 65;
Best Local Similarity 60.0%; Pred. No. 7.8;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLMWITQCF 10
| | | | |
Db 6 LTMWYARCF 15

RESULT 5
Q9PX35 PRELIMINARY; PRT; 152 AA.
AC Q9PX35;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BT-PA96, R1, AND P1;
RX MEDLINE=99394666; PubMed=10466790;
RA Balasuriya U.B.R., Hedges J.F., Nadler S.A., McCollum W.H.,
RA Timoney P.J., MacLachlan N.J.;
RT "Genetic Stability of Equine Arteritis Virus during Horizontal and
RT Vertical Transmission in an Outbreak of Equine Viral Arteritis.";
RL J. Gen. Virol. 80:1949-1958(1999).
DR EMBL; AF118781; AAD54755.1; -.
DR EMBL; AF118773; AAD54707.1; -.
DR EMBL; AF118775; AAD54719.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
SQ SEQUENCE 152 AA; 17150 MW; 5E47F3CD85E193B4 CRC64;

Query Match 66.7%; Score 38; DB 12; Length 152;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCF 10
| : | : | : |
Db 143 LVRWVQCYL 152
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RESULT 6
Q9PX34 ID Q9PX34 PRELIMINARY; PRT; 152 AA.
AC Q9PX34;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P2, A2, A3, AND A4;
RX MEDLINE=99394666; PubMed=10466790;
RA Balasuriya U.B., Hedges J.F., Nadler S.A., McCollum W.H.,
RA Timoney P.J., MacLachlan N.J.;
RT "Genetic Stability of Equine Arteritis Virus during Horizontal and
RT Vertical Transmission in an Outbreak of Equine Viral Arteritis.";
RL J. Gen. Virol. 80:1949-1958(1999).
DR EMBL; AF118776; AAD54725.1; -.
DR EMBL; AF118770; AAD54689.1; -.
DR EMBL; AF118771; AAD54695.1; -.
DR EMBL; AF118772; AAD54701.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR SEQUENCE 152 AA; 17124 MW; 5F8FF3D15420985F CRC64;

Query Match 66.7%; Score 38; DB 12; Length 152;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
I: I: I:I
Db 143 LVRWVQCYL 152

RESULT 7
Q9QKH1 ID Q9QKH1 PRELIMINARY; PRT; 152 AA.
AC Q9QKH1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A1;
RX MEDLINE=99394666; PubMed=10466790;
RA Balasuriya U.B., Hedges J.F., Nadler S.A., McCollum W.H.,
RA Timoney P.J., MacLachlan N.J.;
RT "Genetic stability of equine arteritis virus during horizontal and
RT vertical transmission in an outbreak of equine viral arteritis.";
RL J. Gen. Virol. 80:1949-1958(1999).
DR EMBL; AF118769; AAD54683.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR SEQUENCE 152 AA; 16995 MW; 5F8FE7815B70835F CRC64;

Query Match 66.7%; Score 38; DB 12; Length 152;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
I: I: I:I
Db 143 LVRWVQCYL 152

RESULT 8
Q9QKG6 ID Q9QKG6 PRELIMINARY; PRT; 152 AA.
AC Q9QKG6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R2;
RX MEDLINE=99394666; PubMed=10466790;
RA Balasuriya U.B., Hedges J.F., Nadler S.A., McCollum W.H.,
RA Timoney P.J., MacLachlan N.J.;
RT "Genetic stability of equine arteritis virus during horizontal and
RT vertical transmission in an outbreak of equine viral arteritis.";
RL J. Gen. Virol. 80:1949-1958(1999).
DR EMBL; AF118774; AAD54713.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR SEQUENCE 152 AA; 17082 MW; CF18AEEA1B9D756B CRC64;

Query Match 66.7%; Score 38; DB 12; Length 152;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
I: I: I:I
Db 143 LVRWVQCYL 152

RESULT 9
Q9QKF2 ID Q9QKF2 PRELIMINARY; PRT; 152 AA.
AC Q9QKF2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RQ;
RX MEDLINE=99394666; PubMed=10466790;
RA Balasuriya U.B., Hedges J.F., Nadler S.A., McCollum W.H.,
RA Timoney P.J., MacLachlan N.J.;
RT "Genetic stability of equine arteritis virus during horizontal and
RT vertical transmission in an outbreak of equine viral arteritis.";
RL J. Gen. Virol. 80:1949-1958(1999).
DR EMBL; AF118782; AAD54761.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR SEQUENCE 152 AA; 17138 MW; OE5AF3C417BC256F CRC64;

Query Match 66.7%; Score 38; DB 12; Length 152;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
I: I: I:I
Db 143 LVRWVQCYL 152

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RESULT 10
Q962M9 ID Q962M9 PRELIMINARY; PRT; 273 AA.
AC Q962M9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PVLH14025_P.
GN PVLH14025C.
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RA Tchavtchitch M., Fischer K., Huestis R., Saul A.;
RT "The sequence of 200 kb portion of a Plasmodium vivax chromosome
RT reveals a high degree of conservation with P. falciparum chromosome
RT 3."
RL Mol. Biochem. Parasitol. 0:0-0(2001).
RL EMBL; AY003872; AAF99451.1; -.
SQ SEQUENCE 273 AA; 32028 MW; 73F0E1666635A30C CRC64;

Query Match 66.7%; Score 38; DB 5; Length 273;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
DB 27 LLWITQCF 35

RESULT 11
Q9KRM7 ID Q9KRM7 PRELIMINARY; PRT; 408 AA.
AC Q9KRM7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN VC1609.
GN VC1609.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AE004238; AAF94763.1; -.
DR TIGR; VC1609; -.
KW Complete proteome.
SQ SEQUENCE 408 AA; 44619 MW; B786CB2501E37C8C CRC64;

Query Match 66.7%; Score 38; DB 16; Length 408;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLMWITQCF 9
DB 345 LWLAQCF 352

RESULT 12
O02168 ID O02168 PRELIMINARY; PRT; 423 AA.
AC O02168;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 47.5 KDA PROTEIN.
GN T20F7.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Miller N., Gattung S.;
RT "The sequence of C. elegans cosmid T20F7."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97550; AAK18981.2; -.
KW Hypothetical protein.
SQ SEQUENCE 423 AA; 47451 MW; 6997065D515E7B21 CRC64;

Query Match 66.7%; Score 38; DB 5; Length 423;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLMWITQCF 9
DB 43 LLWITQCF 50

RESULT 13
Q9SGP2 ID Q9SGP2 PRELIMINARY; PRT; 996 AA.
AC Q9SGP2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE F3M18.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palz C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F3M18 from chromosome
RT 1."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

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-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

```
CC EMBL; AC010155; AAF16764.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR; 22.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 18.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 996 AA; 108929 MW; 9C9A6A708A1F933A CRC64;

Query Match 66.7%; Score 38; DB 10; Length 996;
Best Local Similarity 55.6%; Pred. No. 97;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LLMWITQCF 10
Db 209 VMLTECHL 217

RESULT 14
Q9WGD6 PRELIMINARY; PRT; 83 AA.
ID Q9WGD6
AC Q9WGD6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE E5 PROTEIN.
GN E5.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IS808;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-IS808;
RX MEDLINE=99190418; PubMed=10091997;
RA Eriksson A., Herron J.R., Yamada T., Wheeler C.M.;
RT "Human papillomavirus type 16 variant lineages characterized by
RT nucleotide sequence analysis of the E5 coding segment and the E2 hinge
RT region.";
RL J. Gen. Virol. 80:595-600(1999).
DR EMBL; AF120707; AAD24035.1; -.
DR InterPro; IPR004270; Papilloma_E5.
DR Pfam; PF03025; Papilloma_E5; 1.
SQ SEQUENCE 83 AA; 9387 MW; B57D5D3DD77CB7E CRC64;

Query Match 65.8%; Score 37.5; DB 12; Length 83;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 0; Indels 5; Gaps 1;

Qy 1 LLMWIT-----QCFL 10
Db 47 LLLWITTAASAFRCFL 61

Query Match 64.9%; Score 37; DB 5; Length 317;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9
Db 51 IFIWIQCF 59
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Search completed: July 16, 2002, 07:59:50
Job time: 833 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:39:52 ; Search time 113.12 Seconds
(without alignments)
9.819 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWTRQCFLL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	57	100.0	10	20	AAV06003
2	57	100.0	10	21	AAV52434
3	57	100.0	11	19	AAW62585
4	57	100.0	11	20	AAV01761
5	57	100.0	11	21	AAW08702
6	57	100.0	11	21	AAW22790
7	57	100.0	11	21	AAW02630
8	57	100.0	11	21	AAV78469
9	57	100.0	11	21	AAV52431
10	57	100.0	11	22	AAW67165
11	57	100.0	11	22	AAE07777

12	57	100.0	11	22	AAE06849	Human NY-ESO-1 ant
13	57	100.0	11	22	AAW85298	HLA-A2 binding NY-
14	57	100.0	11	22	AAE02119	NY-ESO-1 human leu
15	57	100.0	11	22	AAU01536	Cytolytic T cell 1
16	57	100.0	11	22	AAW82016	HLA-A2 binding pep
17	57	100.0	11	22	AAW69947	Human NY-ESO-1 CTL
18	57	100.0	11	22	AAW33328	Exemplary antigen
19	57	100.0	14	22	AAE07758	Human NY ESO-1 pro
20	57	100.0	14	22	AAE07759	Human HLA-DP restr
21	57	100.0	14	22	AAE07764	Human HLA-DP restr
22	57	100.0	14	22	AAE07765	Human HLA-DP restr
23	57	100.0	14	22	AAE07766	Human HLA-DP restr
24	57	100.0	14	22	AAE07767	Human modified NY
25	57	100.0	14	22	AAE07768	Human modified NY
26	57	100.0	20	22	AAE07744	Human ESO p156-175
27	57	100.0	27	22	AAE07757	Human HLA-DP restr
28	57	100.0	180	19	AAW69664	Human LAGE-1 clone
29	57	100.0	180	19	AAW69665	Human NY-ESO-1 pro
30	57	100.0	180	19	AAW62584	Cancer associated
31	57	100.0	180	20	AAW05965	Human cancer antig
32	57	100.0	180	21	AAW03154	Human oesophageal
33	57	100.0	180	21	AAW70860	Human LAGE-1 splic
34	57	100.0	180	21	AAW70862	Human tumour antig
35	57	100.0	180	21	AAW52430	Human tumour antig
36	57	100.0	180	22	AAW67164	Amino acid sequenc
37	57	100.0	180	22	AAE07714	Human NY-ESO-1 pro
38	57	100.0	180	22	AAU01535	Human NY-ESO-1 tum
39	57	100.0	180	22	AAW69946	Human NY-ESO-1 pro
40	57	100.0	397	22	AAE13122	NY-ESO-1C-HER-2 me
41	53	93.0	9	20	AAV06032	Human cancer antig
42	53	93.0	9	20	AAV06033	Human cancer antig
43	53	93.0	9	21	AAV79756	NY-ESO-1 derived p
44	53	93.0	9	22	AAW67170	Cancer testis tumo
45	53	93.0	9	22	AAW67171	Cancer testis tumo

ALIGNMENTS

RESULT 1
AAV06003
ID AAY06003 standard; Peptide; 10 AA.
XX
AC AAY06003;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.

XX Homo sapiens.

XX WO9918206-A2.

PD 15-APR-1999.

XX 21-SEP-1998; 98WO-US19609.

PR 08-OCT-1997; 97US-0061428.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rosenberg SA, Wang RF;

XX WPI; 1999-277270/23.

PT Cancer antigen NY ESO1/CAG-3
 PS Example 10; Page 42; 88pp; English.
 XX
 CC This peptide was identified as an HLA peptide motif following a
 CC screen for epitopes from the coding region of human ESO-1/CAG-3
 CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
 CC The present peptide (ranked 16) corresponds to amino acid residues
 CC 158-167 of CAG-1 ORF1 (see AAY05985). CAG-1 is a new and potent
 CC tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides (see AAY05967-87) derived from
 CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
 CC vaccines. A claimed method of preventing or inhibiting cancer
 CC involves administering a cancer peptide, with or without an HLA
 CC molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 57; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLMWITQCFL 10
 Db 1 llmwitqcfl 10
 RESULT 2
 AAY52434
 ID AAY52434 standard; peptide; 10 AA.
 XX
 AC AAY52434;
 XX
 XX 15-FEB-2000 (first entry)
 DT Human tumour antigen NY-ESO-1 peptide #7.
 DE
 DE
 XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class I;
 KW T-cell; cytotoxic; stimulation; proliferation; treatment;
 KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
 KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
 KW lymphoma.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W0953938-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US06875.
 XX
 PR 17-APR-1998; 98US-0062422.
 PR 02-OCT-1998; 98US-0165546.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
 PI Gure A, Ritter G;
 XX
 DR WPI; 2000-038483/03.
 XX
 XX Novel peptides which bind to MHC class I and MHC class II molecules,
 PT useful for therapeutic and diagnostic purposes -
 XX
 PS Claim 55; Page 20; 49pp; English.
 XX

CC Peptides #4-#7 (AAY52431-Y52434) are peptides derived from the human
 CC tumour antigen, NY-ESO-1 (AAY52430) which contain the motif LLMWIT
 CC (AAY52441). These sequences can bind to MHC (major histocompatibility
 CC class I HLA-A2 molecules, thereby stimulating proliferation of
 CC cytotoxic T-cells. cDNA encoding NY-ESO-1 was initially isolated
 CC from an oesophagus squamous cell cancer cDNA library. Tissue
 CC localisation studies revealed it to be expressed at high levels
 CC in normal ovary and testis but not in normal colon, kidney, liver,
 CC brain, oesophagus and skin. It was expressed in certain tumours and
 CC tumour cell lines with some degree of frequency - these included
 CC melanoma specimens and cell lines, and breast and bladder cancer
 CC specimens, with expression in other tumour types being sporadic.
 CC These NY-ESO-1-derived peptides may be used in methods and
 CC compositions used for the treatment, diagnosis and prevention of
 CC cancers (such as melanoma, breast cancer, prostate cancer, lung
 CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
 CC or lymphoma) and to stimulate the proliferation of T cells.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 57; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLMWITQCFL 10
 Db 1 llmwitqcfl 10
 RESULT 3
 AAW62585
 ID AAW62585 standard; Peptide; 11 AA.
 XX
 AC AAW62585;
 XX
 DT 17-SEP-1998 (first entry)
 DE
 DE Cancer associated antigen peptide.
 XX
 KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
 KW cancer; treatment; diagnosis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09814464-A1.
 XX
 PD 09-APR-1998.
 XX
 PF 15-SEP-1997; 97WO-US16335.
 XX
 PR 03-OCT-1996; 96US-0725182.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Chen Y, Drijfhout JW, Gure A, Jager E, Knuth A;
 PI Old LJ, Scanlan M;
 XX
 DR WPI; 1998-286417/25.
 XX
 XX New isolated cancer associated antigen - is used to develop products
 PT for the diagnosis and treatment of cancers and for monitoring cancer
 PT therapy
 XX
 PS Claim 33; Page 17; 49pp; English.
 XX
 CC Peptides AAW62585-87 are derived from cancer associated antigen
 CC NY-ESO-1, and are stimulators of cytotoxic T-cells. The specification
 CC describes a method for determining regression, progression of onset of a
 CC cancerous condition, comprising monitoring a sample from a patient
 CC with the cancerous condition for a parameter selected from NY-ESO-1
 CC protein, a peptide derived from NY-ESO-1 protein and cytolytic

CC T cells specific for the peptide and an MHC molecule with which it
 CC non-covalently complexes. Methods for the treatment of a cancerous
 CC condition are also described. The NY-ESO-1 protein and peptides derived
 CC from it can be used for diagnosis and treatment of cancers and to
 CC monitor the efficacy of a therapeutic regime.

XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 |||||
 Db 2 llmwitqcfl 11

RESULT 4

AA01761
 ID AAY01761 standard; Peptide; 11 AA.

XX
 AC AAY01761;

DT 25-JUN-1999 (first entry)

XX Exemplary antigenic peptide derived from NY-ESO-1.

XX MAGE-3; tumour associated gene; human leucocyte antigen Class II;
 KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;
 KW osteosarcoma; leukemia; carcinoma.

XX Homo sapiens.

OS
 XX WO9914326-A1.

PN
 XX 25-MAR-1999.

PD
 XX 04-SEP-1998; 98WO-US18601.

PF
 XX 12-SEP-1997; 97US-0928615.

PR
 XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYVR-) UNIV VRIJE BRUSSEL.

PI Boon-Falleur T, Chaux P, Corthals J, Heirman C;

PI Luiten R, Stroobant V, Thielemans K, Van Der Bruggen P;

XX WPI; 1999-244031/20.

DR Isolated peptides that bind to human leucocyte antigen class II
 PT molecules

PT Disclosure; Page 29; 88pp; English.

XX The present sequence represents an exemplary tumour associated peptide
 CC antigen. The specification describes a MAGE-3 tumour associated gene.
 CC Peptides (AAY01721-25) that bind human leucocyte antigen (HLA) Class II
 CC molecules can be derived from the MAGE-3 protein. These peptides and
 CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide
 CC and HLA Class II, are used to treat MAGE-3 related diseases,
 CC particularly cancers (e.g. melanoma, osteosarcoma, leukemia and
 CC various forms of carcinoma). The peptides are also used to produce
 CC specific antibodies. Detection of of the peptides, e.g. in binding
 CC assays, particularly with antibodies, is used for diagnosis of such
 CC diseases.

XX Sequence 11 AA;

Query Match 100.0%; Score 57; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 |||||
 Db 2 llmwitqcfl 11

RESULT 5

AA08702
 ID AAB08702 standard; Peptide; 11 AA.

XX
 AC AAB08702;

XX 02-JAN-2001 (first entry)

DT Antigenic peptide from tumour rejection antigen NY-ESO-1.

XX Epha3; HLA class II-binding peptide; human leucocyte antigen; antigen;
 KW CD4+ T lymphocyte; tumour associated gene; vaccine.

XX Homo sapiens.

OS
 XX WO2000050589-A1.

PN
 XX 31-AUG-2000.

PD 18-FEB-2000; 2000WO-US04326.

PF 22-FEB-1999; 99US-0121170.

PR 08-OCT-1999; 99US-0158566.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Chiari R, Coulie P, Boon-Falleur T;

XX WPI; 2000-572089/53.

XX Novel tyrosine kinase receptor, Epha3 human leukocyte antigen (HLA)
 PT class II binding peptide and nucleic acid encoding the receptor, useful
 PT for diagnosing and treating conditions characterized by expression of
 PT Epha3 gene

PS Disclosure; Page 35; 107pp; English.

XX AAB08668-B08704 represent antigenic peptides characteristic of tumours.
 CC The peptides may be combined in vaccines with a human Epha3 HLA (human
 CC leukocyte antigen) class II-binding peptide. Epha3 antigens, when
 CC presented by an antigen presenting cell having a HLA class II molecule,
 CC effectively induce activation and proliferation of CD4+ T lymphocytes.
 CC Epha3 is a tumour associated gene. Epha3 HLA binding peptides are used
 CC for selectively enriching a population of T lymphocytes. The peptides
 CC are also used for diagnosing a disorder characterized by Epha3 or Epha3
 CC HLA binding peptide expression. The peptides are also used to treat a
 CC disorder characterized by Epha3 expression. The Epha3 binding peptides
 CC are useful in producing vaccines and antibody.

XX Sequence 11 AA;

Query Match 100.0%; Score 57; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 |||||
 Db 2 llmwitqcfl 11

RESULT 6

AA022790
 ID AAB22790 standard; peptide; 11 AA.

XX
 AC AAB22790;

XX

DT XX 22-DEC-2000 (first entry)
DE XX NY-ESO-1 peptide epitope, SEQ ID NO:1.
XX
KW NY-ESO-1; epitope; CTL response; cytotoxic T lymphocyte; vaccine;
KW immunogenic; adjuvant coadministration; microbial infection;
KW tuberculosis; HIV; hepatitis B virus; hepatitis C virus; cancer.
XX
OS Unidentified.
XX
PN WO200048630-A1.
XX
PD 24-AUG-2000.
XX
PF 17-FEB-2000; 2000WO-AU00110.
XX
PR 17-FEB-1999; 99AU-0008735.
XX
PR 27-JUL-1999; 99AU-0001861.
XX
XX (CSLC-) CSL LTD.
PA
XX Cox JC, Drane DP;
XX
XX WPI: 2000-571930/53.
XX
XX Immunogenic complexes comprising negatively charged organic carrier
PT adjuvants and positively charged antigens for use as vaccines against
PT microbial infection and cancer -
XX
XX Example 4; Fig 5a; 11lpp; English.
XX
XX The invention relates to a novel immunogenic complex comprising a
CC charged organic carrier and a charged antigen which are
CC electrostatically associated. The complex induces a cytotoxic T
CC lymphocyte (CTL) response. The complex and/or vaccine can be used to
CC treat a disease in a mammal, where the complex/vaccine elicits, induces
CC or otherwise facilitates an immune response which inhibits, halts, delays
CC or prevents the onset or progression of the disease condition. In
CC particular, the disease is a condition resulting from a microbial
CC infection or cancer. Microbial infections which may be treated using the
CC immunogenic complex include human immunodeficiency virus (HIV), hepatitis
CC B, hepatitis C, tuberculosis or a parasitic condition, and cancers which
CC may be treated include melanoma, prostate cancer or breast cancer. The
CC complexes and vaccines simultaneously co-deliver antigen and adjuvant to
CC the same antigen presenting cell, which is often essential for induction
CC of appropriate immune responses. Sequences AAB22790-B22791 represent
CC peptide epitopes of the positively charged protein NY-ESO-1 used in an
XX exemplification of the invention.
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 57; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMWITQCFL 10
Db 2 llmwitqcfl 11
|||||
RESULT 7
AAB02630
ID AAB02630 standard; Peptide; 11 AA.
XX
XX AAB02630;
AC
XX 18-AUG-2000 (first entry)
DT
XX
XX Tumour associated peptide antigen from NY-ESO-1 #1.
DE
XX
XX MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;
KW cancer; human; tumour; tumour associated gene product.

XX Homo sapiens.
OS
XX WO200020581-A1.
XX
XX 13-APR-2000.
PD
XX
XX 15-SEP-1999; 99WO-US21230.
PF
XX
XX 05-OCT-1998; 98US-0166448.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYVR-) UNIV VRIJE BRUSSEL.
PA
XX Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;
PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Cortals J;
PI Heirman C;
XX
XX WPI: 2000-317713/27.
DR
XX
XX New MAGE-A3 class II binding peptides, useful to diagnose and treat
PT tumours, are fragments of MAGE-A3 which bind to and are presented to T
PT lymphocytes by human leukocyte antigen class II molecules -
XX
XX Disclosure; Page 33; 119pp; English.
XX
XX The present invention relates to MAGE-A3 (tumour associated gene
CC product) human leukocyte antigen (HLA) class II-binding peptides (see
CC AAB02566-B02595, and AAB02633-B02637). These peptides are presented to T
CC cells in the context of HLA class II molecules. The peptides stimulate
CC the activity and proliferation of CD4+ T lymphocytes. The invention also
CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928
CC and AAA37938-A37940). The peptides and nucleotide sequences can be used
CC to create antibodies against the MAGE-A3 peptides, the antibodies,
CC peptides and nucleotide sequences can be used to create a vaccine. The
CC peptides are used to diagnose or treat a disorder characterized by
CC expression of MAGE-3, particularly cancer. The methods can also be used
CC in the diagnosis of disorders associated with MAGE-3 expression. Included
CC in the invention are other human tumour antigens (see AAB02596-B02637),
CC and PCR primers used in the course of the invention (see AAA37929-A37937
CC and AAA37941-A37942).
XX
XX Sequence 11 AA;
SQ
Query Match 100.0%; Score 57; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMWITQCFL 10
Db 2 llmwitqcfl 11
|||||
RESULT 8
AAY78469
ID AAY78469 standard; Peptide; 11 AA.
XX
XX AAY78469;
AC
XX 10-MAY-2000 (first entry)
DT
XX
XX NY-ESO-1 derived peptide #1.
DE
XX
XX Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1;
KW HLA binding; human leukocyte antigen; cytolytic T cell; CTL;
KW cytostatic; melanoma; synovial sarcoma.
XX
XX Homo sapiens.
OS
XX WO200000824-A1.
PN
XX 06-JAN-2000.
XX

```

XX 25-JUN-1999; 99WO-US14493.
XX
XX 26-JUN-1998; 98US-0105839.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Tureci O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S;
PI Chen Y, Gure A, Old LJ;
XX WPI; 2000-170933/15.
XX
XX Determining the possible presence of breast, endometrial, colorectal,
PT lung, bladder or head-neck cancer -
XX
XX Example 12; Page 21; 40pp; English.
XX
XX A method has been developed for determining the possible presence of a
CC cancer, which is not melanoma or synovial sarcoma. The method comprises
CC assaying a sample taken from the subject to determine the expression of
CC an SSX gene, and determining the expression as a determination of the
CC possible presence of cancer. Expression of SSX1 gene indicates possible
CC presence of breast, endometrial, colorectal, lung, bladder or head-neck
CC cancer. These cancers are also detected by SSX2 and SSX4 gene
CC expression. SSX2 gene expression additionally indicates possible presence
CC of lymphoma, renal cell cancer, glioma and prostate cancer. Expression
CC of SSX4 gene also indicates possible presence of ovarian or stomach
CC cancer. SSX5 gene expression indicates the same cancers as SSX1, except
CC breast cancer. Determining expression of SSX gene can be used to monitor
CC progress of melanoma or synovial sarcoma, which is not cancer. The
CC SSX-derived peptide complex stimulates proliferation of cytolytic T
CC cells. This is useful for treating cancer, especially melanoma. AAY78464
CC to AAY78468 represent specifically claimed HLA binding peptides for use
CC in the method of the invention. AAZ88452 to AAZ88465 represent PCR
CC primers used in the isolation of SSX genes in the exemplification of the
CC present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762
CC represent peptides derived from SSX proteins or NY-ESO-1, which are used
CC in the exemplification of the present invention.
XX
XX Sequence 11 AA;
SQ

```

Query Match 100.0%; Score 57; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 1 LLMWITQCFL 10
Db 2 llmwitqcfl 11

```

RESULT 9
AAY52431
ID AAY52431 standard; peptide; 11 AA.
XX
XX AAY52431;
XX
XX 15-FEB-2000 (first entry)
XX
XX Human tumour antigen NY-ESO-1 peptide #4.
XX
XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class I;
XX T-cell; cytotoxic; stimulation; proliferation; treatment;
XX diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
XX prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
XX lymphoma.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9593938-A1.
XX
XX 28-OCT-1999.

```

XX 24-MAR-1999; 99WO-US06875.
XX
XX 17-APR-1998; 98US-0062422.
XX
XX 02-OCT-1998; 98US-0165546.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
XX WPI; 2000-038483/03.
XX
XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX
XX Claim 60; Page 18; 49pp; English.
XX
XX Peptides #4-#7 (AAY52431-Y52434) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAY52430) which contain the motif LLMWIT
CC (AAY52441). These sequences can bind to MHC (major histocompatibility
CC Class I HLA-A2 molecules, thereby stimulating proliferation of
CC cytotoxic T-cells. cDNA encoding NY-ESO-1 was initially isolated
CC from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
XX Sequence 11 AA;
SQ

```

Query Match 100.0%; Score 57; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 LLMWITQCFL 10
Db 2 llmwitqcfl 11

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RESULT 10
AAG67165
ID AAG67165 standard; peptide; 11 AA.
XX
XX AAG67165;
XX
XX 13-NOV-2001 (first entry)
XX
XX Cancer testis tumour antigen NY-ESO-1 derived CTL-stimulating peptide.
XX
XX Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
XX HLA; HLA binding peptide; major histocompatibility complex; MHC;
XX tumour; cancer; testis tumour.
XX
XX Homo sapiens.
XX
XX WO200162917-A1.
XX
XX 30-AUG-2001.
XX
XX 22-JAN-2001; 2001WO-US02126.
XX
XX 22-FEB-2000; 2000US-0510635.
XX
XX (LUDW-) LUDWIG INST CANCER RES.

XX Lethe B, Boon-Falleur T;
 XX WPI; 2001-550091/61.
 XX Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
 PT for diagnosing testicular tumours -
 XX Example 12; Page 24; 50pp; English.
 XX The present sequence represents a peptide which is derived from cancer
 CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptide
 CC stimulates cytolytic T cell lines (CTLs). NY-ESO-1 is a molecule that
 CC is processed to at least one human leukocyte antigen (HLA) binding
 CC peptide, which binds to Class I and Class II major histocompatibility
 CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
 CC but not normal colon, kidney, liver or brain tissue. The presence or
 CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
 CC cancer, especially testis tumours.
 XX SQ Sequence 11 AA;
 Query Match 100.0%; Score 57; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLMWITQCFL 10
 DB 2 llmwitqcfl 11
 RESULT 11
 AAEE07777
 ID AAE07777 standard; peptide; 11 AA.
 XX AC AAE07777;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human wildtype NY ESO-1 peptide, ESOp157-167.
 XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX OS Homo sapiens.
 XX PN WO20015393-A2.
 XX PD 02-AUG-2001.
 XX PF 26-JAN-2001; 2001WO-US02765.
 XX PR 28-JAN-2000; 2000US-0179004.
 XX PR 29-SEP-2000; 2000US-0237107.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Wang R, Rosenberg SA, Zeng G;
 XX WPI; 2001-496851/54.
 XX DR New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis -
 XX Example 14; Page 62; 134pp; English.
 XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II

CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any
 CC given target antigen and/or hapten and to induce tumour-specific
 CC humoral-mediated immunity against cancer. The present sequence is human
 CC wildtype NY ESO-1 peptide, ESOp157-167.
 XX SQ Sequence 11 AA;
 Query Match 100.0%; Score 57; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLMWITQCFL 10
 DB 2 llmwitqcfl 11
 RESULT 12
 AAEE06849
 ID AAE06849 standard; peptide; 11 AA.
 XX AC AAE06849;
 XX DT 16-OCT-2001 (first entry)
 XX DE Human NY-ESO-1 antigenic peptide #1.
 XX KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;
 KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;
 KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;
 KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;
 KW gene therapy; tumour rejection antigen; TRA; human; NY-ESO-1;
 KW MHC; major histocompatibility complex.
 XX OS Homo sapiens.
 XX PN WO200153833-A1.
 XX PD 26-JUL-2001.
 XX PF 19-JAN-2001; 2001WO-US02008.
 XX PR 20-JAN-2000; 2000US-0177242.
 XX PR 25-OCT-2000; 2000US-0243212.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;
 PI Demotte N, Schultz E;
 XX WPI; 2001-488724/53.
 XX DR Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or
 PT HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used
 PT in diagnosis and treatment of a disorder characterized by expression of
 PT MAGE-A1 or -A3 -
 XX Disclosure; Page 28; 103pp; English.
 XX The invention relates to functional variants and isolated mimetics of a
 CC MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide,
 CC or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described

in the specification. MAGE genes encode tumour rejection antigens (TRAs) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules. The MAGE antigenic peptide acts by binding to HLA molecules on tumour cells and stimulating recognition of these cells and thus signalling them to the immune system for destruction. The peptide when presented by HLA molecule induces the activation and stimulation of CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to treat and diagnose disorders characterised by expression of MAGE-A1 or -A3. Disorders include cancers e.g melanomas, oesophageal, lung, head and neck, breast, colorectal, prostate, renal, bladder, hepatocellular, papillary thyroid and gastric carcinomas, myelomas, brain tumours, sarcomas, seminomas, and ovarian tumours. The present sequence is human NY-ESO-1 tumour associated antigenic peptide presented by major histocompatibility complex (MHC) HLA-A2. The antigenic peptide is used in combination with peptides of the invention for inducing an immune response.

Sequence 11 AA;

Query Match 100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 lllmwitqcfl 11

RESULT 13
AAB85298
ID AAB85298 standard; peptide; 11 AA.
AC AAB85298;
XX
XX
DT 17-SEP-2001 (first entry)
XX
DE HLA-A2 binding NY-ESO-1 peptide #1.
XX
KW NY-ESO-1; human leukocyte antigen; HLA; lysis; cytolytic T cell; CTL;
KW HLA-A2; T-cell sorter; tumor; immune tetramer.
XX
OS Homo sapiens.
XX
PN WO200136453-A2.
XX
PD 25-MAY-2001.
XX
PF 08-NOV-2000; 2000WO-US42010.
XX
PR 15-NOV-1999; 99US-0440621.
PR 25-FEB-2000; 2000US-0514036.
PR 23-SEP-2000; 2000US-0676005.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYOX-) UNIV OXFORD.
XX
PI Valmori D, Cerottini J, Romero P, Cerundolo V;
XX
DR WPI; 2001-451454/48.
XX
XX Novel isolated NY-ESO-1 nonapeptide useful for determining if a cell
PT presents human leukocyte antigen-A2 molecule on its surface, binds to
PT human leukocyte antigen molecules and provokes lysis by cytolytic T
PT cells -
XX
XX Example 1; Page 4; 38pp; English.
PS
XX The invention provides NY-ESO-1 peptide derivatives which bind to human
CC leukocyte antigen (HLA) molecules and provokes lysis by cytolytic T cells
CC (CTLs). The NY-ESO-1 nonapeptide is of formula LLMWITQX, where X is an
CC amino acid having an uncharged polar side chain. The NY-ESO-1 peptide
CC derivatives are useful for determining if a cell presents an HLA-A2

molecule on its surface, by contacting a sample containing the cell with the peptide or its derivative, and determining binding between them, CC where the binding is indicative of HLA-A2 on the surface of the cell.
CC The NY-ESO-1 peptides and analogues are useful therapeutically, for CC administration to a patient who is HLA-A2 positive and expresses NY-ESO-1 CC in connection with the pathology, as well as diagnostically, i.e. to CC determine if HLA-A2 positive cells are present, or if relevant CTLs are CC present. They are also useful for determining the presence of CTLs in a CC sample. The peptides are useful as T-cell sorters, when incorporated into CC immune tetramers. The present sequence represents a NY-ESO-1 peptide that CC can bind to HLA-A2 molecule.

Sequence 11 AA;

Query Match 100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 lllmwitqcfl 11

RESULT 14
AAE02119
ID AAE02119 standard; peptide; 11 AA.
XX
AC AAE02119;
XX

DT 31-JUL-2001 (first entry)

DE NY-ESO-1 human leukocyte antigen-A2-binding peptide #1.

XX Human; cytostatic; immunogen; NY-ESO-1; human leukocyte antigen;
KW HLA; CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
KW brain tumour; sarcoma; vaccine; gene therapy.
XX

OS Homo sapiens.

XX WO200129220-A2.

PN 26-APR-2001.

XX 19-OCT-2000; 2000WO-US28852.

XX 19-OCT-1999; 99US-0160374.

PR 01-FEB-2000; 2000US-0179570.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;

DR WPI; 2001-328498/34.

XX New antigenic peptides derived from MAGE-A12 polypeptides, useful for
PT diagnosis and treatment of cancer, such as bladder, lung, breast,
PT brain, prostate and renal carcinomas -

XX Disclosure; Page 21; 69pp; English.

XX The patent discloses antigenic peptides derived from MAGE-A12
CC protein and presented by human leukocyte antigens (HLAs). These
CC antigenic peptides when presented by an antigen presenting cell
CC having a HLA class I molecule, effectively induce the activation
CC and proliferation of CD8+ cytotoxic T lymphocytes (CTLs). MAGE-A12
CC is useful for treating a subject having a disorder characterised by
CC expression of MAGE-A12. The protein microarray comprising MAGE-A12
CC is useful for diagnosing a disorder, especially cancer, by determining
CC the binding of an antibody, T lymphocytes or a HLA molecule isolated
CC from the subject suspected of having the disorder characterised by the
CC expression of MAGE-A12. MAGE-A12 is useful for treating cancers,
CC including bladder carcinomas, melanomas, oesophageal, lung, head and

CC neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
CC prostate and renal carcinomas and to produce antibodies. MAGE-A12
CC antibodies are useful for diagnosing disorders characterised by
CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-A12 peptides
CC are used as vaccines. They are also used in gene therapy.
CC The present sequence is an antigenic peptide derived from NY-ESO-1. This
CC peptide which is characteristic of tumours is presented by HLA-A2 MHC
CC (major histocompatibility complex) and is recognised by CTLs.

XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 llmwitqcfl 11
|||||

RESULT 15
AAU01536
ID AAU01536 standard; Peptide; 11 AA.
XX
AC AAU01536;
XX
DT 18-JUL-2001 (first entry)
XX
DE Cytolytic T cell line stimulator peptide #1.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody; cytolytic T cell line.

XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US26411.
XX
PR 29-SEP-1999; 99US-0408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -
XX
PS Example 12; Page 17; 62pp; English.
XX

CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which efficiently stimulates cytolytic T cell lines.
CC NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major
CC histocompatibility complex (MHC) Class II molecules such as human
CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
CC proliferation of helper T cells. The peptides can be administered to an
CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
CC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
CC or present in free form is useful for this stimulation. The nucleic acid
CC is useful for screening for a cancerous condition, which involves
CC contacting a subject sample to a cell line transfected with the
CC immunoreactive cell (helper T cell), where interaction is indicative of
CC cancer. In addition, a sample from a patient (for example, a body fluid

CC or tissue) can be monitored for the amount of the complex present in the
CC bloodstream. This is useful for determining regression, progression or
CC onset of a cancerous condition. The method involves contacting the sample
CC with a radioactive labelled or enzyme labelled monoclonal antibody which
CC specifically binds with the complex.

XX Sequence 11 AA;

Query Match 100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 llmwitqcfl 11
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Search completed: July 16, 2002, 07:45:50
Job time: 358 sec

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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:43:02 ; Search time 477.3 Seconds
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7.374 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
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Scoring table: BLOSUM62
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Searched: 3502263 seqs, 351980561 residues
Total number of hits satisfying chosen parameters: 3502263

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	15	US-09-165-546A-7
2	57	100.0	10	19	US-09-529-206-92
3	57	100.0	10	19	US-09-529-206A-92
4	57	100.0	10	19	US-09-529-206B-92
5	57	100.0	11	1	PCT-US00-04326-42
6	57	100.0	11	1	PCT-US99-06875-4
7	57	100.0	11	15	US-09-165-546A-4

8	57	100.0	11	17	US-09-336-091-41	Sequence 41, Appl
9	57	100.0	11	17	US-09-396-315-79	Sequence 79, Appl
10	57	100.0	11	18	US-09-408-036B-4	Sequence 4, Appl
11	57	100.0	11	18	US-09-440-621-1	Sequence 1, Appl
12	57	100.0	11	19	US-09-510-635A-4	Sequence 4, Appl
13	57	100.0	11	19	US-09-574-749-33	Sequence 33, Appl
14	57	100.0	11	20	US-09-676-005B-1	Sequence 1, Appl
15	57	100.0	11	20	US-09-692-401-43	Sequence 43, Appl
16	57	100.0	11	20	US-09-697-884-79	Sequence 79, Appl
17	57	100.0	11	21	US-09-705-160-42	Sequence 42, Appl
18	57	100.0	11	21	US-09-751-798-4	Sequence 4, Appl
19	57	100.0	11	21	US-09-766-889A-50	Sequence 50, Appl
20	57	100.0	11	23	US-09-913-756-42	Sequence 4, Appl
21	57	100.0	11	24	US-10-023-182-4	Sequence 17, Appl
22	57	100.0	122	26	US-60-336-968-17	Sequence 7, Appl
23	57	100.0	180	11	US-08-791-495-7	Sequence 9, Appl
24	57	100.0	180	11	US-08-791-495-9	Sequence 9, Appl
25	57	100.0	180	17	US-09-341-829A-7	Sequence 7, Appl
26	57	100.0	180	17	US-09-341-829A-9	Sequence 9, Appl
27	57	100.0	180	17	US-09-392-714-25	Sequence 25, Appl
28	57	100.0	180	19	US-09-529-206-4	Sequence 4, Appl
29	57	100.0	180	19	US-09-529-206A-3	Sequence 3, Appl
30	57	100.0	180	19	US-09-529-206B-3	Sequence 3, Appl
31	57	100.0	180	19	US-09-561-571-3	Sequence 3, Appl
32	57	100.0	180	21	US-09-751-798-8	Sequence 8, Appl
33	57	100.0	180	24	US-10-005-905-3	Sequence 3, Appl
34	57	100.0	180	24	US-10-023-182-8	Sequence 8, Appl
35	57	100.0	180	24	US-10-026-066-3	Sequence 3, Appl
36	57	100.0	180	26	US-60-336-968-11	Sequence 11, Appl
37	57	100.0	397	22	US-09-821-883-27	Sequence 27, Appl
38	53	93.0	9	18	US-09-409-455A-123	Sequence 123, Appl
39	53	93.0	9	19	US-09-529-206-71	Sequence 71, Appl
40	53	93.0	9	19	US-09-529-206-72	Sequence 72, Appl
41	53	93.0	9	19	US-09-529-206A-71	Sequence 71, Appl
42	53	93.0	9	19	US-09-529-206A-72	Sequence 72, Appl
43	53	93.0	9	19	US-09-529-206B-71	Sequence 71, Appl
44	53	93.0	9	19	US-09-529-206B-72	Sequence 72, Appl
45	53	93.0	9	22	US-09-833-039-123	Sequence 123, App

ALIGNMENTS

RESULT 1

US-09-165-546A-7
; Sequence 7, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10158

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546A
FILING DATE: 02-Oct-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998

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; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-165-546A-7

Query Match          100.0%; Score 57; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 1 LLMWITQCFL 10

RESULT 2
US-09-529-206-92
; Sequence 92, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: The Government of the United States of America as
; FILE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-92

Query Match          100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 1 LLMWITQCFL 10

RESULT 3
US-09-529-206A-92
; Sequence 92, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
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; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-92

Query Match          100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 1 LLMWITQCFL 10

RESULT 4
US-09-529-206B-92
; Sequence 92, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-92

Query Match          100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 1 LLMWITQCFL 10

RESULT 5
PCT-US00-04326-42
; Sequence 42, Application PC/TUS00004326
; GENERAL INFORMATION:
; APPLICANT: Chiali, Rita
; APPLICANT: Coulie, Pierre G.
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TYROSINE KINASE RECEPTOR EphA3 ANTIGENIC PEPTIDES
; FILE REFERENCE: L0461/7057W0
; CURRENT APPLICATION NUMBER: PCT/US00/04326
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: US 60/121,170
; EARLIER FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: US 60/158,566
; EARLIER FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
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PCT-US00-04326-42

Query Match 100.0%; Score 57; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
 |||||
Db 2 LLMWITQCFL 11

RESULT 6

PCT-US99-06875-4
; Sequence 4, Application PC/TUS9906875
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/06875
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear

PCT-US99-06875-4
Query Match 100.0%; Score 57; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
 |||||
Db 2 LLMWITQCFL 11

RESULT 7

US-09-165-546A-4
; Sequence 4, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/06875
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear

Qy 1 LLMWITQCFL 10
 |||||
Db 2 LLMWITQCFL 11

RESULT 8

US-09-336-091-41
; Sequence 41, Application US/09336091
; GENERAL INFORMATION:
; APPLICANT: Van Snick, Jacques
; APPLICANT: Leth, Bernard
; APPLICANT: Chaux, Pascal
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-A1 PEPTIDES PRESENTED BY HLA CLASS
; TITLE OF INVENTION: II MOLECULES
; FILE REFERENCE: L0461/7063
; CURRENT APPLICATION NUMBER: US/09/336,091
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41

; GENERAL INFORMATION:

APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
MHC CLASS I AND MHC CLASS II MOLECULES, AND
USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: FULBRIGHT & JAWORSKI LLP

STREET: 666 Fifth Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10158

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,546A

FILING DATE: 02-Oct-1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/062,422

FILING DATE: April 17, 1998

APPLICATION NUMBER: 08/937,263

FILING DATE: September 15, 1997

APPLICATION NUMBER: US 08/752,182

FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, Norman D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5466.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-165-546A-4

Query Match 100.0%; Score 57; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10

|||||

Db 2 LLMWITQCFL 11

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-091-41

Query Match 100.0%; Score 57; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
Db 2 LLMWITQCFL 11

RESULT 9

US-09-396-315-79
; Sequence 79, Application US/09396315
; GENERAL INFORMATION:
; APPLICANT: Schultz, Erwin S.
; APPLICANT: Van Snick, Jacques
; APPLICANT: Leth, Bernard
; APPLICANT: Chaux, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Kurthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7067
; CURRENT APPLICATION NUMBER: US/09/396,315
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-396-315-79

Query Match 100.0%; Score 57; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
Db 2 LLMWITQCFL 11

RESULT 10

US-09-408-036B-4
; Sequence 4, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendschuh, Michael
; TITLE OF INVENTION: Isolated Peptides which Bind to MHC Class II Molecules and Uses Thereof
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-4

Query Match 100.0%; Score 57; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
Db 2 LLMWITQCFL 11

RESULT 11

US-09-440-621-1
; Sequence 1, Application US/09440621
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerottini, Jean-Charles
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629
; CURRENT APPLICATION NUMBER: US/09/440,621
; CURRENT FILING DATE: 1999-11-15
; EARLIER APPLICATION NUMBER: US 09/165,546
; EARLIER FILING DATE: 1998-10-02
; EARLIER APPLICATION NUMBER: US 09/062,422
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/725,162
; EARLIER FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-440-621-1

Query Match 100.0%; Score 57; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
Db 2 LLMWITQCFL 11

RESULT 12

US-09-510-635A-4
; Sequence 4, Application US/09510635A
; GENERAL INFORMATION:
; APPLICANT: Bernard Leth, and Thierry Boon-Falleur
; TITLE OF INVENTION: ISOLATED GENOMIC SEQUENCES WHICH ENCODE NY-ESO-1 AND USES THEREOF
; FILE REFERENCE: LUD 5633
; CURRENT APPLICATION NUMBER: US/09/510,635A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-2
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-510-635A-4

Query Match 100.0%; Score 57; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
Db 2 LLMWITQCFL 11

RESULT 13

US-09-574-749-33
; Sequence 33, Application US/09574749
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7006
; CURRENT APPLICATION NUMBER: US/09/574,749
; CURRENT FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749-33

Query Match 100.0%; Score 57; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
| | | | | | | | | |
Db 2 LLMWITQCFL 11

RESULT 14

US-09-676-005B-1
; Sequence 1, Application US/09676005B
; GENERAL INFORMATION:
; APPLICANT: Valmorli, Danila
; APPLICANT: Cerrotini, Jean, Charels
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.2
; CURRENT APPLICATION NUMBER: US/09/676,005B
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US09/514,036
; PRIOR FILING DATE: 2000-02-05
; PRIOR APPLICATION NUMBER: US09/440,621
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 09/165,546
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 09/062,422
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 08/725,162
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-676-005B-1

Query Match 100.0%; Score 57; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
| | | | | | | | | |
Db 2 LLMWITQCFL 11

RESULT 15
US-09-692-401-43
; Sequence 43, Application US/09692401
; GENERAL INFORMATION:
; APPLICANT: Heidecker, Leonora
; APPLICANT: van den Eynde, Benot
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Brasseur, Francis
; TITLE OF INVENTION: MAGE-A12 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: L0461/7097
; CURRENT APPLICATION NUMBER: US/09/692,401
; CURRENT FILING DATE: 2000-10-19
; EARLIER APPLICATION NUMBER: US 60/160,374
; EARLIER FILING DATE: 1999-10-19
; EARLIER APPLICATION NUMBER: US 60/179,570
; EARLIER FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-692-401-43

Query Match 100.0%; Score 57; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
| | | | | | | | | |
Db 2 LLMWITQCFL 11

Search completed: July 16, 2002, 07:56:35
Job time: 813 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:43:42 ; Search time 63.47 Seconds
(without alignments)
17.524 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 344541 seqs, 111227333 residues

Total number of hits satisfying chosen parameters: 344541

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New: *
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep: *
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep: *
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep: *
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep: *
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep: *
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep: *
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	57	100.0	11 5	US-09-344-040C-130
2	57	100.0	11 5	US-09-574-749B-33
3	57	100.0	11 6	US-10-177-277-130
4	57	100.0	28 6	US-10-117-937-255
5	57	100.0	180 1	PCT-US02-13994-30
6	57	100.0	180 5	US-09-807-512-4
7	57	100.0	180 5	US-09-807-512-8
8	57	100.0	180 6	US-10-117-937-74
9	57	100.0	180 6	US-10-117-937-75
10	57	100.0	180 6	US-10-146-473-69
11	53	93.0	9 5	US-09-344-040C-123
12	53	93.0	9 6	US-10-177-277-123
13	47	82.5	9 1	PCT-US02-05748-24
14	47	82.5	9 5	US-09-344-040C-131
15	47	82.5	9 5	US-09-670-456A-1
16	47	82.5	9 5	US-09-574-749B-34
17	47	82.5	9 6	US-10-117-937-197
18	47	82.5	9 6	US-10-177-277-131
19	44	77.2	9 6	US-10-117-937-196
20	38	66.7	9 1	PCT-US02-05748-25
21	38	66.7	462 7	US-60-360-039-4233
22	38	66.7	986 7	US-60-382-898-110
23	37	64.9	125 1	PCT-US02-09921-971
24	36	63.2	176 5	US-09-935-625-10391
25	36	63.2	205 5	US-09-935-625-10389
26	36	63.2	259 5	US-09-935-625-9112

27	36	63.2	297	5	US-09-935-625-9111	Sequence 9111, Ap
28	36	63.2	343	5	US-09-935-625-9110	Sequence 9110, Ap
29	36	63.2	1054	7	US-60-360-039-1918	Sequence 1918, Ap
30	36	63.2	1156	5	US-09-935-625-9116	Sequence 9116, Ap
31	36	63.2	1194	5	US-09-935-625-9115	Sequence 9115, Ap
32	36	63.2	1240	5	US-09-935-625-9114	Sequence 9114, Ap
33	35	61.4	492	7	US-60-360-039-2801	Sequence 2801, Ap
34	35	61.4	635	5	US-09-540-209B-8038	Sequence 8038, Ap
35	34	59.6	86	6	US-10-117-477-67	Sequence 67, Appl
36	34	59.6	89	6	US-10-117-477-35	Sequence 35, Appl
37	34	59.6	93	6	US-10-155-881-7745	Sequence 7745, Ap
38	34	59.6	275	1	PCT-US02-10159-4	Sequence 4, Appl
39	34	59.6	275	6	US-10-112-645-4	Sequence 4, Appl
40	34	59.6	307	1	PCT-US02-09921-643	Sequence 643, App
41	34	59.6	357	6	US-10-104-047-3115	Sequence 3115, Ap
42	34	59.6	504	7	US-60-360-039-5799	Sequence 5799, Ap
43	34	59.6	1008	6	US-10-155-881-30322	Sequence 30322, A
44	33	57.9	9	1	PCT-US02-05748-26	Sequence 26, Appl
45	33	57.9	9	5	US-09-344-040C-122	Sequence 122, App

ALIGNMENTS

RESULT 1
US-09-344-040C-130
; Sequence 130, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: fureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Expression of an Ssx Gene, Peptides Derived From Said Ssx Gen
; TITLE OF INVENTION: Expression of an Ssx Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 130
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-130

Query Match 100.0%; Score 57; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
Db 2 LLMWITQCFL 11

RESULT 2
US-09-574-749B-33
; Sequence 33, Application US/09574749B
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B

; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-33

Query Match 100.0%; Score 57; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
DB 2 LLMWITQCFL 11

RESULT 3

US-10-177-277-130
; Sequence 130, Application US/10177277
; GENERAL INFORMATION:

; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 130
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-130

Query Match 100.0%; Score 57; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
DB 2 LLMWITQCFL 11

RESULT 4

US-10-117-937-255
; Sequence 255, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping

; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-255

Query Match 100.0%; Score 57; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
DB 9 LLMWITQCFL 18

RESULT 5

PCT-US02-13994-30
; Sequence 30, Application PC/TUS0213994
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; APPLICANT: Scanlan, Elisabeth
; APPLICANT: Stockert, Matthias
; TITLE OF INVENTION: COLON CANCER ANTIGEN PANEL
; FILE REFERENCE: L00461/70105WQ(JRV)
; CURRENT APPLICATION NUMBER: PCT/US02/13994
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US 09/849,602
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-13994-30

Query Match 100.0%; Score 57; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
DB 158 LLMWITQCFL 167

RESULT 6

US-09-807-512-4
; Sequence 4, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1

; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807.512
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-4

Query Match 100.0%; Score 57; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 158 LLMWITQCFL 167

RESULT 7
US-09-807-512-8
; Sequence 8, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; FILE REFERENCE: 0652.2200000
; CURRENT APPLICATION NUMBER: US/09/807.512
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT/EP99/07832
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP 98119583.7
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-512-8

Query Match 100.0%; Score 57; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 158 LLMWITQCFL 167

RESULT 8
US-10-117-937-74
; Sequence 74, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117.937
; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match 100.0%; Score 57; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 158 LLMWITQCFL 167

RESULT 9
US-10-117-937-75
; Sequence 75, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117.937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-75

Query Match 100.0%; Score 57; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 158 LLMWITQCFL 167

RESULT 10
US-10-146-473-69
; Sequence 69, Application US/10146473
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)

; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-69

Query Match 100.0%; Score 57; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | |
DB 158 LLMWITQCFL 167

RESULT 11
US-09-344-040C-123
; Sequence 123, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-123

Query Match 93.0%; Score 53; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCFL 10
| | | | | | | |
DB 1 LLMWITQCFL 9

RESULT 12
US-10-177-277-123
; Sequence 123, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-123

Query Match 93.0%; Score 53; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCFL 10
| | | | | | | |
DB 1 LLMWITQCFL 9

RESULT 13
PCT-US02-05748-24
; Sequence 24, Application PC/TUS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-05748-24

Query Match 82.5%; Score 47; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
| | | | | | | |
DB 2 LLMWITQC 9

RESULT 14
US-09-344-040C-131
; Sequence 131, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130

; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-131

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
| | | | |
Db 2 LLMWITQC 9

RESULT 15
US-09-670-456A-1
; Sequence 1, Application US/09670456A
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjjatic, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-456A-1

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
| | | | |
Db 2 LLMWITQC 9

Search completed: July 16, 2002, 07:58:00
Job time: 858 sec

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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:41:32 ; Search time 45.25 Seconds
(without alignments)
5.398 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	10	4	US-09-359-503-7
2	57	100.0	11	4	US-09-183-931-42
3	57	100.0	11	4	US-09-359-503-4
4	57	100.0	11	4	US-09-062-422-4
5	57	100.0	11	4	US-08-937-263B-4
6	57	100.0	11	4	US-09-166-448-79
7	57	100.0	180	2	US-08-791-495-7
8	57	100.0	180	2	US-08-791-495-9
9	57	100.0	180	4	US-08-937-263B-8
10	47	82.5	9	4	US-09-183-931-43
11	47	82.5	9	4	US-09-359-503-5
12	47	82.5	9	4	US-09-062-422-5
13	47	82.5	9	4	US-08-937-263B-5
14	47	82.5	9	4	US-09-166-448-80
15	35.5	62.3	20	2	US-08-934-915-84
16	35	61.4	527	1	US-08-805-814-10
17	35	61.4	527	1	US-08-484-815-10
18	35	61.4	527	3	US-08-888-949-10
19	35	61.4	527	4	US-08-888-950-10
20	35	61.4	527	4	US-09-262-758-10
21	35	61.4	527	5	PCT-US95-10284-10
22	33	57.9	6	4	US-09-359-503-14
23	33	57.9	6	4	US-09-062-422-7
24	33	57.9	6	4	US-08-937-263B-7
25	33	57.9	9	4	US-09-183-931-44
26	33	57.9	9	4	US-09-359-503-6
27	33	57.9	9	4	US-09-062-422-6

28	33	57.9	9	4	US-08-937-263B-6	Sequence 6, Appli
29	33	57.9	9	4	US-09-166-448-81	Sequence 81, Appli
30	33	57.9	49	1	US-08-118-270-202	Sequence 202, App
31	33	57.9	49	5	PCT-US93-08528-202	Sequence 202, App
32	33	57.9	498	1	US-08-496-855A-6	Sequence 6, Appli
33	33	57.9	498	2	US-08-466-589-12	Sequence 12, Appl
34	33	57.9	498	2	US-08-700-636-12	Sequence 12, Appl
35	33	57.9	498	3	US-08-467-574-12	Sequence 12, Appl
36	33	57.9	498	4	US-09-217-345-12	Sequence 12, Appl
37	33	57.9	1054	1	US-07-596-467-4	Sequence 4, Appli
38	33	57.9	1054	1	US-07-934-374-4	Sequence 4, Appli
39	33	57.9	1054	1	US-07-783-861C-2	Sequence 2, Appli
40	33	57.9	3118	2	US-08-457-273B-8	Sequence 8, Appli
41	33	57.9	3119	1	US-08-246-982A-16	Sequence 16, Appl
42	33	57.9	3119	1	US-08-453-265-16	Sequence 16, Appl
43	32.5	57.0	1239	2	US-08-937-931-2	Sequence 2, Appli
44	32.5	57.0	1239	4	US-09-285-502-2	Sequence 2, Appli
45	32.5	57.0	1239	4	US-09-709-126-2	Sequence 2, Appli

RESULT 1
US-09-359-503-7
; Sequence 7, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

```
;
; TOPOLOGY: linear
; US-09-359-503-7

Query Match      100.0%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
   |||||
Db 1 LLMWITQCFL 10

RESULT 2
US-09-183-931-42
; Sequence 42, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527 1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018,422
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 42
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-183-931-42

Query Match      100.0%; Score 57; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
   |||||
Db 2 LLMWITQCFL 11

RESULT 3
US-09-359-503-4
; Sequence 4, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, Alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; APPLICATION DATA:
; ON NUMBER: US/09/359,503
; FILE: July 23, 1999
; APPLICATION DATA:
; to NY-

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-4

Query Match      100.0%; Score 57; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
   |||||
Db 2 LLMWITQCFL 11

RESULT 4
US-09-062-422-4
; Sequence 4, Application US/09062422
; Patent No. 6252052
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,422
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
```

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Db      2  LLMWITQCFL 11
|||||
RESULT      6
US-09-166-448-79
; Sequence 79, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Failleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgan
; TITLE OF INVENTION: MAG-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-79

Query Match      100.0%; Score 57; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY      1  LLMWITQCFL 10
|||||
Db      2  LLMWITQCFL 11

RESULT      7
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Failleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441

```



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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 180 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-791-495-7

Query Match      100.0%; Score 57; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 158 LLMWITQCFL 167

RESULT 8
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Failleu, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 180 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-791-495-9

Query Match      100.0%; Score 57; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 158 LLMWITQCFL 167

RESULT 9
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 180
;   TYPE: amino acid
;   TOPOLOGY: linear
; US-08-937-263B-8

Query Match      100.0%; Score 57; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 158 LLMWITQCFL 167

RESULT 10
US-09-183-931-43
; Sequence 43, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Failleu, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527.1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018,422
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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OTHER INFORMATION:
US-09-183-931-43

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
|||||||
Db 2 LLMWITQC 9

RESULT 11

US-09-359-503-5
; Sequence 5, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM

OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546

FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263

FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.

REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1

TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids
TYPE: amino acid

TOPOLOGY: linear
US-09-359-503-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
|||||||

Db 2 LLMWITQC 9

RESULT 12

US-09-062-422-5
; Sequence 5, Application US/09062422
; Patent No. 6252052
; GENERAL INFORMATION:

APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
APPLICANT: Old, Lloyd J

TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED

TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue
CITY: New York City

STATE: New York
COUNTRY: USA

ZIP: 10022
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM

OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,422

FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263

FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6252052man D.

REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3

TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids
TYPE: amino acid

TOPOLOGY: linear
US-09-062-422-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
|||||||

Db 2 LLMWITQC 9

RESULT 13

US-08-937-263B-5
; Sequence 5, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;

APPLICANT: Alexander, Knuth; Drifhout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE

TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
ITSELF, AND USES THEREOF

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-937-263B-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
|||||||
DB 2 LLMWITQC 9

RESULT 14
US-09-166-448-80
Sequence 80, Application US/09166448
Patent No. 6291430
GENERAL INFORMATION:
APPLICANT: Chau, Pascal
APPLICANT: Vantomme, Valrie
APPLICANT: Stroobant, Vincent
APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Thielemans, Kris
APPLICANT: Cortals, Jurgan
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
FILE REFERENCE: L0461/7052
CURRENT APPLICATION NUMBER: US/09/166,448
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 80
LENGTH: 9
TYPE: PPT
ORGANISM: Homo sapiens
US-09-166-448-80

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8

Db 2 LLMWITQC 9
|||||||

RESULT 15
US-08-934-915-84
Sequence 84, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-84

Query Match 62.3%; Score 35.5; DB 2; Length 20;
Best Local Similarity 46.7%; Pred. No. 6.3;
Matches 7; Conservative 3; Mismatches 0; Indels 5; Gaps 1;

QY 1 LLMWIT-----QCFL 10
|||:|
DB 1 LLLWITAASAFRCFI 15

Search completed: July 16, 2002, 07:46:56
Job time: 324 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:58:07 ; Search time 14.82 Seconds
(without alignments)
64.838 Million cell updates/sec

Title: US-09-165-546A-7

Perfect score: 57

Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 28138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1099

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	22	38.6	10	2 PT0289	Ig heavy chain CRD
2	20	35.1	7	2 S09652	hypothetical prote
3	20	35.1	7	2 PX0008	glucuronosyltransf
4	20	35.1	9	2 S07241	litorin - Rohde's
5	20	35.1	10	2 T17075	cytochrome-c oxida
6	19	33.3	8	2 S19288	acylase - Kluysera
7	18	31.6	9	2 A29477	diuretic neuropept
8	18	31.6	9	2 I52974	seminal vesicle pr
9	17	29.8	5	2 B45525	actin I - malaria
10	17	29.8	7	2 S08606	hypothetical prote
11	17	29.8	9	2 A28495	conopressin G - co
12	17	29.8	9	2 S39040	lysine-conopressin
13	17	29.8	10	2 T13976	cytochrome-c oxida
14	16	28.1	8	2 A61364	acetylcholinestera
15	16	28.1	9	2 PC2021	isotocin - common
16	16	28.1	9	2 S27873	oxytocin-related p
17	16	28.1	10	2 S27873	hypothetical prote
18	16	28.1	10	2 PT0310	Ig heavy chain CRD
19	16	28.1	10	2 E41946	T-cell receptor ga
20	16	28.1	10	2 T17057	cytochrome-c oxida
21	16	28.1	10	2 T12303	cytochrome-c oxida
22	16	28.1	10	2 T14019	cytochrome-c oxida
23	16	28.1	10	2 T17060	cytochrome-c oxida
24	16	28.1	10	2 T12325	cytochrome-c oxida
25	16	28.1	10	2 T17072	cytochrome-c oxida
26	16	28.1	10	2 T12312	cytochrome-c oxida
27	15	26.3	6	2 F41946	T-cell receptor ga
28	15	26.3	7	2 A61081	tryptophyllin, bas
29	15	26.3	8	2 T13818	cytochrome oxidase

30 15 26.3 9 2 JS0302 xenopsin-related p
31 15 26.3 9 2 A60320 xenopsin-related p
32 15 26.3 9 2 PT0231 Ig heavy chain CDR
33 15 26.3 9 2 S78426 52.5K protein - sp
34 15 26.3 10 2 I44644 neurotoxin-associa
35 15 26.3 10 2 E49033 T-cell receptor ga
36 15 26.3 10 2 T13838 cytochrome-c oxida
37 15 26.3 10 2 T17066 cytochrome-c oxida
38 15 26.3 10 2 T17069 cytochrome-c oxida
39 15 26.3 10 2 T14219 cytochrome-c oxida
40 14 24.6 5 2 A60803 neuropeptide - sea
41 14 24.6 5 2 S65726 hemoglobin, extrac
42 14 24.6 6 2 PT0641 T-cell receptor be
43 14 24.6 7 2 S19630 ribosomal protein
44 14 24.6 7 2 A58512 venom heptapeptide
45 14 24.6 7 2 A34026 acetylcholinestera

ALIGNMENTS

RESULT 1

PT0289

Ig heavy chain CRD3 region (clone 4-109) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0289

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A;Reference number: PT0222; MUID:91108337

A;Accession: PT0289

A;Molecule type: DNA

A;Residues: 1-10 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 38.6%; Score 22; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWIT 6

Db 1 LLNWIS 6

RESULT 2

S09652

hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)

C;Species: Enterobacter cloacae

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999

C;Accession: S09652

R;Vlieghehart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.

Antimicrob. Agents Chemother. 33, 1153-1159, 1989

A;Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant i

A;Reference number: S09651; MUID:90024972

A;Accession: S09652

A;Molecule type: DNA

A;Residues: 1-7 <VLI>

A;Cross-references: EMBL:X51534; NID:g40878; PIDN:CAA35914.1; PID:g581034

Query Match 35.1%; Score 20; DB 2; Length 7;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWI 5

Db 1 MIWI 5

RESULT 3

PX0008

glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)

N:Alternate names: UDP-glucuronosyltransferase

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997

C:Accession: PX0008

R:Yokota, H.; Yuasa, A.; Sato, R.

J. Biochem. 104, 531-536, 1988

A:Title: Purification and properties of a form of UDP-glucuronosyltransferase from liver

A:Reference number: PX0008; MUID:89197852

A:Accession: PX0008

A:Molecule type: protein

A:Residues: 1-7 <YOK>

C:Keywords: glucosyltransferase; hexosyltransferase; liver

Query Match 35.1%; Score 20; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMW 4

Db 3 LLWV 6

RESULT 4

S07241

Litorin - Rohde's leaf frog

C:Species: Phyllomedusa rohdei (Rohde's leaf frog)

C:Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C:Accession: S07241

R:Barra, D.; Falconieri Erspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Erspamer,

FEBS Lett. 182, 53-56, 1985

A:Title: Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.

A:Reference number: S07241; MUID:85127560

A:Accession: S07241

A:Molecule type: protein

A:Residues: 1-9 <BAR>

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.1%; Score 20; DB 2; Length 9;
Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 MWITQCF 10

Db 2 LWATGHFM 9

RESULT 5

T17075

cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)

C:Species: mitochondrion Chamaeleo fischeri

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999

C:Accession: T17075

R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A:Title: Evolutionary shifts in three major structural features of the mitochondrial gen

A:Reference number: T18674; MUID:97315309

A:Accession: T17075

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <MAC>

A:Cross-references: EMBL:U82688; NID:g3603112; PID:g3603115; PIDN:AAG62275.1

C:Genetics:

A:Genome: mitochondrion

A:Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match 35.1%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWI 5

Db 3 LLRWL 7

RESULT 6

S19288

acylase - Kluyvera cryocrescens

C:Species: Kluyvera cryocrescens

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S19288

R:Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.

Biochem. J. 280, 659-662, 1991

A:Title: Chemical modification of serine at the active site of penicillin acylase fro

A:Reference number: S19288; MUID:92109664

A:Accession: S19288

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <MAR>

Query Match 33.3%; Score 19; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 MWI 5

Db 3 MWV 5

RESULT 7

A29477

diuretic-neuropeptide F1 - migratory locust

C:Species: Locusta migratoria (migratory locust)

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Dec-1993

C:Accession: A29477

R:Proux, J.P.; Miller, C.A.; Li, J.P.; Carney, R.L.; Girardie, A.; Delaage, M.; Schoo

Biochem. Biophys. Res. Commun. 149, 180-186, 1987

A:Title: Identification of an arginine vasopressin-like diuretic hormone from Locusta

A:Reference number: A29477; MUID:88077077

A:Accession: A29477

A:Molecule type: protein

A:Residues: 1-9 <PRO>

A:Note: two neuropeptides, F1 and F2, were identified. F2 is an antiparallel dimer of

C:Keywords: neuropeptide

Query Match 31.6%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ITQC 8

Db 3 ITNC 6

RESULT 8

I52974

seminal vesicle protein IV - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: I52974

R:Teng, C.T.; Harris, S.E.

DNA 2, 105-111, 1983

A:Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive si

A:Reference number: I52974; MUID:83261204

A:Accession: I52974

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-9 <RES>
A:Cross-references: GB:M27324; NID:g207124; PIDN:AAA63501.1; PID:g207125
C:Genetics:
A:Gene: SVSIV

Query Match 31.6%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 MWITQCL 10
I : I I I
Db 1 MKLTSIFL 8

RESULT 9

B45525
actin I - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C:Accession: B45525
R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmaker, M.; Biochem. Parasitol. 35, 167-176, 1989
A:Title: Stage-specific expression and genomic organization of the actin genes of the malaria parasite Plasmodium falciparum
A:Reference number: B45525; MUID:89364996
A:Accession: B45525
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-5 <WES>
A:Cross-references: GB:J03988
A:Note: The authors translated the codon GAA for residue 3 as Gly
C:Comment: The actin I gene contains no introns.

Query Match 29.8%; Score 17; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 QCF 9
I : I
Db 3 ECF 5

RESULT 10

S08606
Hypothetical protein 2 estrogen receptor 5'-region - chicken
C:Species: Gallus gallus (chicken)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
C:Accession: S08606
R:Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.; EMBO J. 5, 891-897, 1986
A:Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oestrogen receptor
A:Reference number: S07192; MUID:86247578
A:Accession: S08606
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-7 <KRU>
A:Cross-references: EMBL:X03805; NID:G63378; PIDN:CAA27432.1; PID:g584490
C:Superfamily: unassigned leader peptides

Query Match 29.8%; Score 17; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQC 8
I : I
Db 1 MFLAHC 6

RESULT 11

A28495

conopressin G - cone shell (Conus geographus)
N:Alternate names: Lys-conopressin-G
C:Species: Conus geographus (geography cone)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 25-Apr-1997
C:Accession: A28495
R:Cruz, L.J.; de Santos, V.; Zafaralla, G.C.; Ramillo, C.A.; Zeikus, R.; Gray, W.R.; O J. Biol. Chem. 262, 15821-15824, 1987
A:Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from the cone shell of Conus geographus
A:Reference number: A92617; MUID:88058932
A:Accession: A28495
A:Molecule type: protein
A:Residues: 1-9 <CRU>
C:Superfamily: oxytocin-neurophysin
C:Keywords: amidated carboxyl end; venom
F:1-6/Disulfide bonds: #status experimental
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.8%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CFL 10
I : I
Db 1 CFI 3

RESULT 12

S39040
lysine-conopressin - Erpobdella octoculata
C:Species: Erpobdella octoculata
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C:Accession: S39040
R:Salzet, M.; Bulet, P.; van Dorsselaer, A.; Malecha, J.; Eur. J. Biochem. 217, 897-903, 1993
A:Title: Isolation, structural characterization and biological function of a lysine-conopressin from the leech Erpobdella octoculata
A:Reference number: S39040; MUID:94039146
A:Accession: S39040
A:Molecule type: protein
A:Residues: 1-9 <SAL>

Query Match 29.8%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CFL 10
I : I
Db 1 CFI 3

RESULT 13

T13976
cytochrome-c oxidase (EC 1.9.3.1) chain I - Cnemidophorus tigris mitochondrion (fragment)
C:Species: mitochondrion Cnemidophorus tigris
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T13976
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.; Mol. Biol. Evol. 14, 91-104, 1997
A:Title: Two novel gene orders and the role of light-strand replication in rearrangement of the cytochrome-c oxidase subunit I gene in the lizard Cnemidophorus tigris
A:Reference number: Z17789; MUID:97153826
A:Accession: T13976
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: EMBL:U71332; NID:g1753236; PID:g1753239; PIDN:AAB48274.1
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 29.8%; Score 17; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 5.9e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 MWITQCF 9
| | | |
Db 1 MTITRWF 7

RESULT 14

A41117
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
C:Species: Naja naja oxianna (Asian cobra, Oxiu cobra)
C:Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 23-Jun-1993
C:Accession: A41117
R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
Proq. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
A:Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a
A:Reference number: A41117; MUID:91296772
A:Accession: A41117
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <KRE>
C:Keywords: carboxylic ester hydrolase

Query Match 28.1%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MW 4
| |
Db 4 MW 5

RESULT 15

A61364
isotocin - common carp
C:Species: Cyprinus carpio (common carp)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
C:Accession: A61364
R:Acher, R.; Chauvet, J.; Chauvet, M.T.; Crepy, D.
Comp. Biochem. Physiol. A 14, 245-254, 1965
A:Title: Caracterisation des hormones neurohypophysaires d'un poisson osseux d'eau douce
A:Reference number: A61364
A:Accession: A61364
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <ACH>
C:Superfamily: oxytocin-neurophysin
C:Keywords: amidated carboxyl end; neuropeptide; posterior pituitary
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.1%; Score 16; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WITQC 8
| | | |
Db 2 YISNC 6

Search completed: July 16, 2002, 08:02:42
Job time: 275 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:02:07 ; Search time 11.74 Seconds
(without alignments)
32.981 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 349

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	35.1	9	1 LITR_PHYRO	P08946 phyllomedusa
2	18	31.6	9	1 DNFL_LOCMI	P18339 locusta mig
3	17	29.8	9	1 CONO_CONGE	P05486 conus geogr
4	16	28.1	9	1 ISOT_CYPCA	P42993 cyprinus ca
5	16	28.1	9	1 OXYT_EISFO	P42998 eisenia foe
6	16	28.1	9	1 OXYT_RAJGL	P42994 raja clavata
7	15	26.3	5	1 UF01_MOUSE	P38639 mus musculus
8	15	26.3	9	1 MGMT_BOVIN	P23177 bos taurus
9	15	26.3	9	1 OXYA_SCYCA	P42996 scyllorhinu
10	15	26.3	9	1 OXYA_SQUAC	P42999 squalus aca
11	15	26.3	10	1 APE_CAPGI	P80474 capnocytoph
12	15	26.3	10	1 RCA_PINPS	P81084 pinus pinas
13	14	24.6	8	1 CPD1_ENTFA	P13269 enterococu
14	14	24.6	9	1 COVN_CONVE	P83047 conus ventr
15	14	24.6	9	1 OXYT_BUFRE	P42995 bufo regula
16	14	24.6	9	1 OXYT_CYPCA	P23879 cyprinus ca
17	14	24.6	9	1 OXYT_RABIT	P32878 oryctolagus
18	14	24.6	9	1 OXYV_SQUAC	P43000 squalus aca
19	13	22.8	6	1 E101_LITRU	P82096 litoria rub
20	13	22.8	9	1 DI_NEPNO	P24816 nephrops no
21	13	22.8	9	1 LITO_LITAU	P08945 litoria aur
22	13	22.8	10	1 GON1_PETWA	P20378 petromyzon
23	13	22.8	10	1 GON3_ONCKE	P20367 oncorhynch
24	13	22.8	10	1 GONL_SQUAC	P27429 squalus aca
25	13	22.8	10	1 LABA_JATMU	P13270 jatropha mu
26	13	22.8	10	1 MP2_MITOC	P81533 microplitis
27	13	22.8	10	1 N040_TOBAC	P55962 nicotiana t
28	13	22.8	10	1 PORB_METTM	P80901 methanobact
29	12	21.1	7	1 CCF1_ENTFA	P20104 enterococu
30	12	21.1	7	1 WWA1_ACHFU	P35919 achatina fu
31	12	21.1	7	1 WWA2_ACHFU	P35920 achatina fu
32	12	21.1	7	1 WWA3_ACHFU	P35921 achatina fu
33	12	21.1	8	1 AC1_THUAL	P18691 thunnus alb

34	12	21.1	8	1 CCKN_MACEU	P30369 macropus eu
35	12	21.1	9	1 CCAP_CARMA	P38556 carcinus ma
36	12	21.1	9	1 CONO_CONST	P05487 conus stria
37	12	21.1	9	1 OXYE_SCYCA	P42997 scyllorhinu
38	12	21.1	9	1 OXYT_OCTVU	P80027 octopus vul
39	12	21.1	10	1 CAER_LITXA	P56264 litoria xan
40	12	21.1	10	1 FARP_MANSE	P18523 manduca sex
41	12	21.1	10	1 HTFL_ROMMI	P18110 romalea mic
42	12	21.1	10	1 HTF2_CARMO	P11385 carausius m
43	12	21.1	10	1 HTF_NAUCI	P10939 nauphoeta c
44	11	19.3	4	1 OCP3_OCTMI	P58649 octopus min
45	11	19.3	5	1 BPP7_BOTIN	P30425 bothrops in

ALIGNMENTS

RESULT 1					
LITR_PHYRO					
ID	LITR_PHYRO	STANDARD;	PRT;	9 AA.	
AC	P08946;				
DT	01-NOV-1988 (Rel. 09, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Rhodei-litorin.				
OS	Phyllomedusa rohdei (Rohde's leaf frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;				
OC	Phyllomedusa.				
OX	NCBI_TaxID=8394;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=85127560; PubMed=3838283;				
RA	Barra D., Erspamer G.F., Simmaco M., Bossa F., Melchiorri P.,				
RA	Erspamer V.;				
RT	"Rhodei-litorin: a new peptide from the skin of Phyllomedusa rohdei.";				
RL	FEBS Lett. 182:53-56(1985).				
CC	- - SUBCELLULAR LOCATION: Secreted.				
CC	- - SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN				
CC	FAMILY.				
DR	PIR: S07241; S07241.				
DR	InterPro; IPR000874; Bombesin.				
DR	Pfam; PF02044; Bombesin; 1.				
DR	PROSITE; PS00257; BOMBESIN; 1.				
KW	Bombesin family; Amidation.				
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.				
FT	MOD_RES 9 9 AMIDATION.				
SQ	SEQUENCE 9 AA; 1090 MW; 4ECCCIE861ADC377 CRC64;				
Query Match	35.1%;	Score 20;	DB 1;	Length 9;	
Best Local Similarity	37.5%;	Pred. No. 1e+05;			
Matches	3;	Conservative	2;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	3 MWITQCFL 10				
	:				
Db	2 LWAUGHFM 9				
RESULT 2					
DNFL_LOCMI					
ID	DNFL_LOCMI	STANDARD;	PRT;	9 AA.	
AC	P16339;				
DT	01-AUG-1990 (Rel. 15, Created)				
DT	01-AUG-1990 (Rel. 15, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	Locupressin (diuretic neuropeptide F1/F2).				
OS	Locusta migratoria (Migratory locust).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;				
OC	Acridomorpha; Acridoidea; Acrididae; Locusta.				
OX	NCBI_TaxID=7004;				
RN	[1]				


```

RP SEQUENCE.
RC TISSUE-Subesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=88077077; PubMed=3689410;
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
RA Delaage M., Schooley D.A.;
RT "Identification of an arginine vasopressin-like diuretic hormone from
RL Locusta migratoria.";
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC -!- FUNCTION: DIURETIC HORMONE.
CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A29477; A29477.
DR InterPro: IPR000981; Neurohypophys_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Neuropeptide; Amidation.
FT DISULFID 1 6 IN F1.
FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 31.6%; Score 18; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ITQC 8
DB 3 ITNC 6

RESULT 3
CONO_CONGE STANDARD; PRT; 9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
DR InterPro: IPR000981; Neurohypophys_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 29.8%; Score 17; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 8 CFL 10
DB 1 CFI 3

RESULT 4
ISOT_CYPCA STANDARD; PRT; 9 AA.
AC P42993;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Isotocin.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE.
RC TISSUE-Pituitary;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishs.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A61364; A61364.
DR InterPro: IPR000981; Neurohypophys_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 28.1%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WITQC 8
DB 2 YISNC 6

RESULT 5
OXYT_EISFO STANDARD; PRT; 9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common brandling worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE.
RC TISSUE-Pituitary;
RX MEDLINE=94121660; PubMed=8292046;
RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC NEPHRIDIAL FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

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DR PIR: PC2021; PC2021.
DR InterPro: IPR000981; Neurhypophys_horm.
DR Pfam: PF00220; hormone4; 1
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 28.1%; Score 16; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 8 CFL 10
Db 1 CFV 3

RESULT 6
OXYT_RAJCL STANDARD; PRT; 9 AA.
AC P42994;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glutitocin.
OS Raja clavata (Thorback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hypnosqualea; Pristiogorale; Batoidea;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE=66123415; PubMed=5880565;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurohypophyseal peptides: isolation of a new hormone,
RT glutitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
RT the ray (Raja clavata).";
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -!- SIMILARITY: ANTIDIURETIC HORMONE.
CC -!- FUNCTION: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurhypophys_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB455B04B CRC64;

Query Match 28.1%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WITQC 8
Db 2 YISNC 6
RESULT 7
UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2b-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE.
RC TISSUE=Fibroblast.
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
FT NON_TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 WI 5
Db 1 WI 2

RESULT 8
MGMT_BOVIN STANDARD; PRT; 9 AA.
ID MGMT_BOVIN
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
DE methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
CC IRREVERSIBLY INACTIVATED.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
CC [protein]-L-cysteine -> DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro: IPR001497; Methyltransf_1.
DR PROSITE: PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ITQC 8
Db 6 LTPC 9

RESULT 9

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OXVA_SCYCA
ID OXVA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyliorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIN ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurohypophys_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match 26.3%; Score 15; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WITQC 8
:| |
Db 2 YINNC 6

RESULT 10
OXVA_SQUAC
ID OXVA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspargtocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysal hormones, valitocin (Val18-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurohypophys_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.

Query Match 26.3%; Score 15; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WITQC 8
:| |
Db 2 YINNC 6

RESULT 11
APE_CAPGI
ID APE_CAPGI STANDARD; PRT; 10 AA.
AC P80474;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Aminopeptidase (EC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; CFB group; Flavobacteria; Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE.
RX STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt D.A., Greenman J., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
RT factor.";
RL Microbiology 141:3087-3093(1995).
CC -!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
CC TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.
CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE
CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
CC CAVITY.
CC -!- COFACTOR: REQUIRES MAGNESIUM OR CALCIUM.
KW Hydrolase; Aminopeptidase; Magnesium; Calcium.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 4.1e+03;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMW 4
:| |
Db 4 MLW 6

RESULT 12
RCA_PINPS
ID RCA_PINPS STANDARD; PRT; 10 AA.
AC P81084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ribulose biphosphate carboxylase/oxygenase activase (RuBisCO
DE activase) (RA) (Water stress responsive protein 4) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RX TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
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RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: ACTIVATION OF RUBISCO (RUBULOSE-1,5-BISPHOSPHATE
CC CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
CC CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
CC CARBAMATE STRUCTURE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
CC -!- INDUCTION: BY WATER STRESS.
CC -!- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
KW Chloroplast; ATP-binding.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1171 MW; C0A506D2C72B1EA6 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 QCFL 10
DB 3 QCEL 6

RESULT 13
CPDI_ENTFA
ID CPDI_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sakakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPD1.";
RL Science 226:849-850(1984).
CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOCIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 24.6%; Score 14; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
DB 2 LVMFLS 7

RESULT 14
COVN_CONVE
ID COVN_CONVE STANDARD; PRT; 9 AA.
AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
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DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Raybaudi Massilia G., Schinina M.E., Ascenzi P., Politicelli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RT vermivorous marine snail Conus ventricosus.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- TISSUE SPECIFICITY: Venom.
KW Amidation; Venom; D-amino acid.
FT DISULFID 3 9
FT MOD_RES 5 5 D-TRYPTOPHAN.
FT MOD_RES 9 9 AMIDATION.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 24.6%; Score 14; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 WITQC 8
DB 5 WKPWC 9

RESULT 15
OXYT_BUFRE
ID OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Seritocin.
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
OC Bufo.
OX NCBI_TaxID=8390;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophysial peptide, seritocin ([ser5,ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: DEVOID OF OXYTOCIC ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 983 MW; 17FF476E5A6D04B CRC64;

Query Match 24.6%; Score 14; DB 1; Length 9;
Best Local Similarity 33.3%; Pred. No. 1e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 CFL 10
DB 1 CYI 3

Search completed: July 16, 2002, 08:06:14
Job time: 247 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:01:32 ; Search time 26.12 Seconds
(without alignments)
66.231 Million cell updates/sec

Title: US-09-165-546A-7

Perfect score: 57

Sequence: 1 LLMWITQCFLL 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvrius:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	36.8	8	2	O85406 coxiella bu
2	21	36.8	8	4	Q15890 homo sapien
3	20	35.1	8	5	Q9VRD2 drosophila
4	20	35.1	10	8	O79912 chameleleo f
5	20	35.1	10	8	Q96697 chameleleo d
6	19	33.3	10	6	Q9N1X1 equus cabal
7	19	33.3	10	11	O9ESU5 mus musculu
8	17	29.8	9	4	Q9H326 homo sapien
9	17	29.8	9	9	Q38340 lactococcus
10	17	29.8	10	2	Q48469 klebsiella
11	17	29.8	10	4	Q96QA7 homo sapien
12	17	29.8	10	8	Q9TC98 shinisaurus
13	17	29.8	10	8	P92616 cnemidophor
14	16	28.1	8	8	Q94VJ4 varanus ben
15	16	28.1	8	11	Q9ET18 mus spretus
16	16	28.1	8	11	Q9ET17 mus caroli

17	16	28.1	8	11	Q9ET16	Q9et16 mesocricetu
18	16	28.1	8	11	Q99MNO	Q99mn0 mus musculu
19	16	28.1	8	11	Q62721	Q62721 rattus norv
20	16	28.1	9	2	Q9R9C4	Q9r9c4 borrelia bu
21	16	28.1	9	4	Q9H3Y3	Q9h3y3 homo sapien
22	16	28.1	10	2	Q934S1	Q934s1 thermus the
23	16	28.1	10	5	Q25355	Q25355 locusta mig
24	16	28.1	10	5	Q25356	Q25356 locusta mig
25	16	28.1	10	6	Q9TR47	Q9tr47 bos taurus
26	16	28.1	10	8	Q9ZYV3	Q9zyv3 dipsosaurus
27	16	28.1	10	8	Q9ZYU4	Q9zyu4 sceloporu
28	16	28.1	10	8	Q9ZYT2	Q9zyt2 leioccephalu
29	16	28.1	10	8	P92707	P92707 platysaurus
30	16	28.1	10	8	P92632	P92632 eremias gra
31	16	28.1	10	8	O79891	O79891 crotaphytus
32	16	28.1	10	8	O79894	O79894 gambelia wi
33	16	28.1	10	8	O79909	O79909 sauronalus
34	16	28.1	10	8	O9T8G5	O9t8g5 liolaemus o
35	16	28.1	10	8	Q9B4X0	Q9b4x0 notophthalm
36	16	28.1	10	8	Q958K9	Q958k9 rana boylii
37	16	28.1	10	11	Q61807	Q61807 mus musculu
38	15	26.3	8	12	O9E8Q4	O9e8q4 beet soil-b
39	15	26.3	8	12	Q9DSN5	Q9dsn5 beet soil-b
40	15	26.3	9	4	Q99887	Q99887 homo sapien
41	15	26.3	9	8	Q94V18	Q94v18 varanus ere
42	15	26.3	9	8	Q94VH4	Q94vh4 varanus gla
43	15	26.3	9	8	Q94VE1	Q94vel varanus mer
44	15	26.3	9	8	Q94VD8	Q94vd8 varanus nil
45	15	26.3	9	9	Q38366	Q38366 bacterioph

ALIGNMENTS

RESULT 1

O85406
ID O85406 PRELIMINARY; PRT; 8 AA.
AC O85406; 1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Coxiella group; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NINE MILE PHASE I;
RX MEDLINE=98348442; PubMed=9683477;
RA Willems H., Jaeger C., Baljer G.;
RT "Physical and genetic map of the obligate intracellular bacterium
RT Coxiella burnetii.";
RL J. Bacteriol. 180:3816-3822(1998).
DR EMBL; AF064963; AAD09947.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match 36.8%; Score 21; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMW 4

Db 1 LLLW 4

RESULT 2

Q15890
ID Q15890 PRELIMINARY; PRT; 8 AA.
AC Q15890;

DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE (CLONE XP19G12A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Cooblaugh M.I., Chinault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries.";
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL; L32083; AAA73880.1; -.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

 Query Match 36.8%; Score 21; DB 4; Length 8;
 Best Local Similarity 37.5%; Pred. No. 5.6e+05;
 Matches 3; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

 QY 4 WI--TQCF 9
 I: ||:
 Db 1 WWSQCY 8

 RESULT 3
 Q9VRD2 PRELIMINARY; PRT; 8 AA.
 AC Q9VRD2
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE CG11666 PROTEIN.
 GN CG11666.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballwe R.A., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA LasR P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003569; AAF50870.1; -.
 DR FLYBase; FBgn0040648; CG11666.
 SQ SEQUENCE 8 AA; 1062 MW; ED11B5B044004376 CRC64;

 Query Match 35.1%; Score 20; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 MWI 5
 I: ||:
 Db 1 MWI 3

 RESULT 4
 O79912 PRELIMINARY; PRT; 10 AA.
 AC O79912
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
 GN COI.
 OS Chamaeleo fischeri.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
 OX NCBI_TaxID=51755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97315309; PubMed=9169559;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Evolutionary shifts in three major structural features of the
 RT mitochondrial genome among iguanian lizards.";
 RL J. Mol. Evol. 44:660-674(1997).
 DR EMBL; U02688; AAC62275.1; -.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1319 MW; 5E218E2733640727 CRC64;

 Query Match 35.1%; Score 20; DB 8; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 1 LLMWI 5
 I: ||:
 Db 3 LLRWL 7

 RESULT 5
 Q9G697 PRELIMINARY; PRT; 10 AA.
 ID Q9G697
 AC Q9G697
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).

GN COI.
 OS Chamaeleo dilepis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
 ON NCBI_TaxID=91908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128460; AAG00617.1; -.
 KW Mitochondrion.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1319 MW; 5E218E2733640727 CRC64;

Query Match 35.1%; Score 20; DB 8; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLMWI 5
 Db 3 LRLWL 7

RESULT 6
 Q9N1X1 PRELIMINARY; PRT; 10 AA.
 ID Q9N1X1
 AC Q9N1X1
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE ALCOHOL DEHYDROGENASE 3 (FRAGMENT).
 GN ADH3.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 ON NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20082971; PubMed=10613847;
 RA Caetano A.R., Shive Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
 RA Bowling A.T., Murray J.D.;
 RT "A comparative gene map of the horse (Equus caballus).";
 RL Genome Res. 9:1239-1249(1999).
 DR EMBL; AF134056; AAF31299.1; -.
 FT NON_TER 1
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1144 MW; C4EA25676B02D6DD CRC64;

Query Match 33.3%; Score 19; DB 6; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.3e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WIT 6
 Db 8 WWT 10

RESULT 7
 Q9ESU5 PRELIMINARY; PRT; 10 AA.
 ID Q9ESU5
 AC Q9ESU5

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE FAS DEATH RECEPTOR (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C3H/HE;
 RX MEDLINE=20127858; PubMed=10660538;
 RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,
 RA Yonish-Rouach E., Reisdorf P.;
 RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a
 RT p53-responsive element that is activated by p53 mutants unable to
 RT induce apoptosis.";
 RL J. Biol. Chem. 275:3867-3872(2000).
 DR EMBL; AF282865; AAG02410.1; -.
 KW Receptor.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 33.3%; Score 19; DB 11; Length 10;
 Best Local Similarity 50.0%; Pred. No. 3.3e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMWI 5
 Db 1 MLWI 4

RESULT 8
 Q9H326 PRELIMINARY; PRT; 9 AA.
 ID Q9H326
 AC Q9H326
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE NAD+-DEPENDENT ISOCITRATE DEHYDROGENASE 3 ALPHA SUBUNIT
 DE (FRAGMENT).
 GN IDH3A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Huh T.-L.;
 RT "Structural and functional characterization of the human NAD+-
 RT dependent isocitrate dehydrogenase alpha subunit promoter.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF157515; AAG43379.1; -.
 FT NON_TER 9
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 960 MW; C91CB0437DC7687D CRC64;

Query Match 29.8%; Score 17; DB 4; Length 9;
 Best Local Similarity 50.0%; Pred. No. 5.6e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WITO 7
 Db 6 WISK 9

RESULT 9
 Q38340 PRELIMINARY; PRT; 9 AA.
 ID Q38340
 AC Q38340
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ORF PROTEIN (FRAGMENT).
GN ORF.
OS Lactococcus phage 936.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=39838;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96084945; PubMed=7489923;
RA Waterfield N.R., Lepage R.W., Wilson P.W., Wells J.M.;
RT "The isolation of lactococcal promoters and their use in investigating
bacterial luciferase synthesis in Lactococcus lactis.";
RL Gene 165:9-15(1995).
DR EMBL: Z48181; CAA88226.1; -
FT NON_TER 9
SQ SEQUENCE 9 AA; 1054 MW; 7098B2CEA6D3372B CRC64;

Query Match 29.8%; Score 17; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQC 8
| : ||
Db 1 MELKQC 6

RESULT 10
Q48469
ID Q48469 PRELIMINARY; PRT; 10 AA.
AC Q48469;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NITROGENASE (FRAGMENT).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246546; PubMed=6306580;
RA Shen S.C., Xue Z.T., Kong O.T., Wu Q.L.;
RT "An open reading frame upstream from the nifH gene of Klebsiella
pneumoniae";
RL Nucleic Acids Res. 11:4241-4250(1983).
DR EMBL: X01006; CAA25501.1; -
FT NON_TER 10
SQ SEQUENCE 10 AA; 1173 MW; B130695DDEA6C406 CRC64;

Query Match 29.8%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQC 8
| : ||
Db 1 MTMRQC 6

RESULT 11
Q96QA7
ID Q96QA7 PRELIMINARY; PRT; 10 AA.
AC Q96QA7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BA151A2.1 (CDC42 GUANINE EXCHANGE FACTOR (GEF) 9 (COLLYBISTIN, PEM-2,
HPM-2, KIAA0424)) (FRAGMENT).
DR HPME-2, KIAA0424;
GN ARHGEF9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Whitehead S.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL451106; CAC88408.1; -
FT NON_TER 10
SQ SEQUENCE 10 AA; 1122 MW; 39925CB878640043 CRC64;

Query Match 29.8%; Score 17; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.5e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMWI 5
| : ||
Db 1 MQWI 4

RESULT 12
Q9TG98
ID Q9TG98 PRELIMINARY; PRT; 10 AA.
AC Q9TG98;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Shinisaurus crocodilurus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Shinisauridae;
OC Shinisaurus.
OX NCBI_TaxID=52224;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343613; PubMed=10413621;
RA Macey J.R., Schulte J.A. II, Larson A., Tunney B.S., Orlov N.,
RA Papenfuss T.J.;
RT "Molecular phylogenetics, tRNA evolution, and historical biogeography
in anquid lizards and related taxonomic families";
RL Mol. Phylogenet. Evol. 12:250-272(1999).
DR EMBL: AF085604; AAD51502.1; -
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1290 MW; 1CEE80C9D36411A0 CRC64;

Query Match 29.8%; Score 17; DB 8; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQCF 9
| : || : |
Db 1 MTITRWF 7

RESULT 13
P92616
ID P92616 PRELIMINARY; PRT; 10 AA.
AC P92616;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Cnemidophorus tigris.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincophora; Teliioidea;
OC Teiidae; Cnemidophorus.
OX NCBI_TaxID=52180;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE-97153826; PubMed-9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT "Two novel gene orders and the role of light-strand replication in
RL rearrangement of the vertebrate mitochondrial genome.";
RN Mol. Biol. Evol. 14:91-104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97153820; PubMed-9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RN structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
DR EMBL: U71332; AAB48274.1; -.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1290 MW; 1CEE80C9D36411A0 CRC64;

Query Match 29.8%; Score 17; DB 8; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQCF 9
DB 1 MTITRWF 7

RESULT 14
Q94VJ4 PRELIMINARY; PRT; 8 AA.
AC Q94VJ4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Varanus bengalensis nebulosis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169827;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL: AF407492; AAL10031.1; -.
KW Mitochondrion.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1053 MW; E8B5B9C733640056 CRC64;

Query Match 28.1%; Score 16; DB 8; Length 8;
Best Local Similarity 20.0%; Pred. No. 5.6e+05;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWI 5
DB 1 MIRWL 5

RESULT 15
Q9ET18 PRELIMINARY; PRT; 8 AA.
AC Q9ET18;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NEUROPEPTIDE Y (FRAGMENT).
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

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OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RA Taylor B.A., Wnek C., Phillips S.J.;
RT "Multiple obesity QTLs identified in an intercross between the NZO
RN (New Zealand obese) and the SM (small) mouse strains.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF286200; AAG01474.1; -.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1033 MW; 297685A76AAB1734 CRC64;

Query Match 28.1%; Score 16; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MW 4
DB 7 MW 8

Search completed: July 16, 2002, 08:05:41
Job time: 249 sec
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GenC_{ore} version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2002, 07:48:27 ; Search time 26.34 Seconds
(without alignments)
42.169 Million cell updates/sec

Title: US-09-165-546A-7

Perfect score: 57

Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 135323

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

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2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	20	AA060003 Human cancer antig
2	57	100.0	10	21	AA060032 Human tumour antig
3	53	93.0	9	20	AA060032 Human cancer antig
4	53	93.0	9	20	AA060033 Human cancer antig
5	53	93.0	9	21	AA060033 NY-ESO-1 derived p
6	53	93.0	9	22	AA060033 Cancer testis tumo
7	53	93.0	9	22	AA060033 Cancer testis tumo
8	53	93.0	9	22	AA060033 Human NY-ESO-1 HLA
9	53	93.0	9	22	AA060033 Human NY-ESO-1 HLA
10	53	93.0	10	20	AA060006 Human cancer antig
11	53	93.0	10	22	AA060037 HLA-A2 binding NY-

12	47	82.5	9	19	AA062586	Cancer associated
13	47	82.5	9	20	AA01762	Exemplary antigeni
14	47	82.5	9	21	AA08703	Antigenic peptide
15	47	82.5	9	21	AA022791	NY-ESO-1 peptide e
16	47	82.5	9	21	AA02631	Tumour associated
17	47	82.5	9	21	AA078470	NY-ESO-1 derived p
18	47	82.5	9	21	AA052432	Human tumour antig
19	47	82.5	9	22	AA067166	Cancer testis tumo
20	47	82.5	9	22	AA06850	Human NY-ESO-1 ant
21	47	82.5	9	22	AA085299	HLA-A2 binding NY-
22	47	82.5	9	22	AA02120	NY-ESO-1 human leu
23	47	82.5	9	22	AA01537	Cytolytic T cell 1
24	47	82.5	9	22	AA082017	HLA- binding pepti
25	47	82.5	9	22	AA069948	Human NY-ESO-1 CTL
26	47	82.5	9	22	AA031329	Exemplary antigen
27	47	82.5	10	22	AA085309	HLA-A2 binding NY-
28	47	82.5	10	22	AA085310	HLA-A2 binding NY-
29	44	77.2	10	20	AA06005	Human cancer antig
30	44	77.2	10	22	AA07778	Human NY ESO-1 epi
31	44	77.2	10	22	AA085313	HLA-A2 binding NY-
32	38	66.7	9	22	AA085303	HLA-A2 binding NY-
33	38	66.7	9	22	AA085304	HLA-A2 binding NY-
34	38	66.7	9	22	AA085305	HLA-A2 binding NY-
35	38	66.7	9	22	AA085306	HLA-A2 binding NY-
36	38	66.7	9	22	AA085308	HLA-A2 binding NY-
37	38	66.7	9	22	AA085315	HLA-A2 binding NY-
38	38	66.7	9	22	AA085316	HLA-A2 binding NY-
39	38	66.7	10	22	AA085311	HLA-A2 binding NY-
40	38	66.7	10	22	AA085312	HLA-A2 binding NY-
41	38	66.7	10	22	AA085314	HLA-A2 binding NY-
42	34	59.6	9	22	AA085317	HLA-A2 binding NY-
43	33.5	58.8	10	20	AA06029	Human cancer antig
44	33	57.9	6	19	AA062588	Cancer associated
45	33	57.9	6	21	AA052441	Human tumour antig

ALIGNMENTS

RESULT 1

AA060003

ID AA060003 standard; Peptide; 10 AA.

XX AA060003;

XX

XX 16-AUG-1999 (first entry)

XX

XX Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; human leukocyte antigen; HLA.

XX Homo sapiens.

XX

XX WO9918206-A2.

XX

XX 15-APR-1999.

XX

XX 21-SEP-1998; 98WO-US19609.

XX

XX 08-OCT-1997; 97US-0061428.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

XX Rosenberg SA, Wang RF;

XX WPI; 1999-277270/23.

XX

PT Cancer antigen NY ESO1/CAG-3

PS Example 10; Page 42; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a

CC screen for epitopes from the coding region of human ESO-1/CAG-3

CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.

CC The present peptide (ranked 16) corresponds to amino acid residues

CC 158-167 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent

CC tumour antigen capable of eliciting an antigen specific immune

CC response by T cells. Cancer peptides (see AAY05967-87) derived from

CC CAG-3, portions of CAG-3 and their variants, are useful as cancer

CC vaccines. A claimed method of preventing or inhibiting cancer

CC involves administering a cancer peptide, with or without an HLA

CC molecule. The cancer peptides form part of, or are derived

CC from, cancers such as primary or metastatic melanoma, thymoma,

CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine

CC cancer, cervical cancer, bladder cancer, kidney cancer and

CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and

CC thyroid cancers.

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 20; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.002;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10

DB 1 lllmwtqcfl 10

RESULT 2

AA52434

ID AAY52434 standard; peptide; 10 AA.

XX

AC AAY52434;

XX

XX 15-FEB-2000 (first entry)

DT

XX Human tumour antigen NY-ESO-1 peptide #7.

DE

XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class I;

XX T-cell; cytotoxic; stimulation; proliferation; treatment;

KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;

KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;

KW lymphoma.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN W0953938-A1.

XX

XX 28-OCT-1999.

PD

XX

XX 24-MAR-1999; 99WO-US06875.

PF

XX

XX 17-APR-1998; 98US-0062422.

PR

XX

XX 02-OCT-1998; 98US-0165546.

XX

XX (LUDW-) LUDWIG INST CANCER RES.

PA

XX

XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;

PI Gure A, Ritter G;

PI

XX WPI; 2000-038483/03.

DR

XX

XX Novel peptides which bind to MHC class I and MHC class II molecules,

PT useful for therapeutic and diagnostic purposes

PT

XX

XX Claim 55; Page 20; 49pp; English.

PS

XX

CC Peptides #4-#7 (AAY52431-Y52434) are peptides derived from the human

CC tumour antigen, NY-ESO-1 (AAY52430) which contain the motif LLMWIT

CC (AAY52441). These sequences can bind to MHC (major histocompatibility

CC Class I HLA-A2 molecules, thereby stimulating proliferation of

CC cytotoxic T-cells. cDNA encoding NY-ESO-1 was initially isolated

CC from an oesophagus squamous cell cancer cDNA library. Tissue

CC localisation studies revealed it to be expressed at high levels

CC in normal ovary and testis but not in normal colon, kidney, liver,

CC brain, oesophagus and skin. It was expressed in certain tumours and

CC tumour cell lines with some degree of frequency - these included

CC melanoma specimens and cell lines, and breast and bladder cancer

CC specimens, with expression in other tumour types being sporadic.

CC These NY-ESO-1-derived peptides may be used in methods and

CC compositions used for the treatment, diagnosis and prevention of

CC cancers (such as melanoma, breast cancer, prostate cancer, lung

CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,

CC or lymphoma) and to stimulate the proliferation of T cells.

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.002;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10

DB 1 lllmwtqcfl 10

RESULT 3

AA52432

ID AAY06032 standard; Peptide; 9 AA.

XX

AC AAY06032;

XX

XX 16-AUG-1999 (first entry)

DT

XX

XX Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

DE

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;

KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;

KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;

KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;

KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;

KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;

KW vaccine; human leukocyte antigen; HLA.

XX

OS Homo sapiens.

XX

XX W09918206-A2.

XX

XX 15-APR-1999.

PD

XX

XX 21-SEP-1998; 98WO-US19609.

PF

XX

XX 08-OCT-1997; 97US-0061428.

PR

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA

XX

XX Rosenberg SA, Wang RF;

PI

XX

XX WPI; 1999-277270/23.

DR

XX

XX Cancer antigen NY ESO1/CAG-3

PT

XX

XX Example 10; Page 43; 88pp; English.

PS

XX

XX This peptide was identified as an HLA peptide motif following a

CC screen for epitopes from the coding region of human ESO-1/CAG-3

CC ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.

CC The present peptide (ranked 15) corresponds to amino acid residues

CC 159-167 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent

CC

CC tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides (see AAY05967-87) derived from
 CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
 CC vaccines. A claimed method of preventing or inhibiting cancer
 CC involves administering a cancer peptide, with or without an HLA
 CC molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.
 XX Sequence 9 AA;
 SQ

Query Match 93.0%; Score 53; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITOCFL 10
 Db 1 lmwitqcf 9
 |||||

RESULT 4
 AAY06033
 ID AAY06033 standard; Peptide; 9 AA.

XX AC AAY06033;

XX DT 16-AUG-1999 (first entry)

XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; human leukocyte antigen; HLA.

XX OS Homo sapiens.

XX PN WO9918206-A2.

XX PD 15-APR-1999.

XX PF 21-SEP-1998; 98WO-US19609.

XX PR 08-OCT-1997; 97US-0061428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Rosenberg SA, Wang RF;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3

XX Example 10; Page 43; 88pp; English.

CC This peptide was identified as an HLA peptide motif following a
 CC screen for epitopes from the coding region of human ESO-1/CAG-3
 CC ORF1 (see AAY58599). 30 Epitopes (see AAY06018-47) were identified.
 CC The present peptide (ranked 16) corresponds to amino acid residues
 CC 158-166 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
 CC tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides (see AAY05967-87) derived from
 CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
 CC vaccines. A claimed method of preventing or inhibiting cancer
 CC involves administering a cancer peptide, with or without an HLA
 CC molecule. The cancer peptides form part of, or are derived

CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.
 XX Sequence 9 AA;
 SQ

Query Match 93.0%; Score 53; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITOCF 9
 Db 1 lllmwitqcf 9
 |||||

RESULT 5
 AAY79756
 ID AAY79756 standard; Peptide; 9 AA.

XX AC AAY79756;

XX DT 10-MAY-2000 (first entry)

XX DE NY-ESO-1 derived peptide #12.

XX Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1;
 KW HLA binding; human leukocyte antigen; cytolytic T cell; CTL;
 KW cytostatic; melanoma; synovial sarcoma.

XX OS Homo sapiens.

XX PN WO200000824-A1.

XX PD 06-JAN-2000.

XX PF 25-JUN-1999; 99WO-US14493.

XX PR 26-JUN-1998; 98US-0105839.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Tureci O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S;
 PI Chen Y, Gure A, Old LJ;

XX WPI; 2000-170933/15.

XX Determining the possible presence of breast, endometrial, colorectal,
 PT lung, bladder or head-neck cancer -
 PT

XX Example 13; Page 26; 40pp; English.

XX A method has been developed for determining the possible presence of a
 CC cancer, which is not melanoma or synovial sarcoma. The method comprises
 CC assaying a sample taken from the subject to determine the expression of
 CC an SSX gene, and determining the expression as a determination of the
 CC possible presence of cancer. Expression of SSX1 gene indicates possible
 CC presence of breast, endometrial, colorectal, lung, bladder or head-neck
 CC cancer. These cancers are also detected by SSX2 and SSX4 gene
 CC expression. SSX2 gene expression additionally indicates possible presence
 CC of lymphoma, renal cell cancer, glioma and prostate cancer. Expression
 CC of SSX4 gene also indicates possible presence of ovarian or stomach
 CC cancer. SSX5 gene expression indicates the same cancers as SSX1, except
 CC breast cancer. Determining expression of SSX gene can be used to monitor
 CC progress of melanoma or synovial sarcoma, which is not cancer. The
 CC SSX-derived peptide complex stimulates proliferation of cytolytic T
 CC cells. This is useful for treating cancer, especially melanoma. AAY78464
 CC to AAY78468 represent specifically claimed HLA binding peptides for use
 CC in the method of the invention. AAY88452 to AAY88465 represent PCR
 CC primers used in the isolation of SSX genes in the exemplification of the
 CC present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762

CC represent peptides derived from SSX proteins or NY-ESO-1, which are used
CC in the exemplification of the present invention.

SQ Sequence 9 AA;

Query Match 93.0%; Score 53; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQCF 10
| | | | | | | |
Db 1 lmwtqcf 9

RESULT 6

AAG67170
ID AAG67170 standard; peptide; 9 AA.

AC AAG67170;

DT 13-NOV-2001 (first entry)

DE Cancer testis tumour antigen NY-ESO-1 derived peptide.

XX
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.

OS Homo sapiens.

PN WO200162917-A1.

PD 30-AUG-2001.

XX
XX
PF 22-JAN-2001; 2001WO-US02126.

XX
XX
PR 22-FEB-2000; 2000US-0510635.

XX (LUDW-) LUDWIG INST CANCER RES.

PA Lethe B, Boon-Falleur T;

PI WPI; 2001-550091/61.

XX
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -

PS Example 13; Page 26; 50pp; English.

XX
XX
CC AAG67169-AAG67206 represent peptides which are derived from cancer
CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides
CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that
CC is processed to at least one human leukocyte antigen (HLA) binding
CC peptide, which binds to Class I and Class II major histocompatibility
CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
CC but not normal colon, kidney, liver or brain tissue. The presence or
CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
CC cancer, especially testis tumours.

XX Sequence 9 AA;

Query Match 93.0%; Score 53; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLWITQCF 9
| | | | | | | |
Db 1 llmwitqcf 9

RESULT 7

AAG67171
ID AAG67171 standard; peptide; 9 AA.

XX
AC AAG67171;

DT 13-NOV-2001 (first entry)

DE Cancer testis tumour antigen NY-ESO-1 derived peptide.

XX
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.

OS Homo sapiens.

PN WO200162917-A1.

PD 30-AUG-2001.

XX
XX
PF 22-JAN-2001; 2001WO-US02126.

XX
XX
PR 22-FEB-2000; 2000US-0510635.

XX (LUDW-) LUDWIG INST CANCER RES.

PA Lethe B, Boon-Falleur T;

PI WPI; 2001-550091/61.

XX
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -

PS Example 13; Page 26; 50pp; English.

XX
XX
CC AAG67169-AAG67206 represent peptides which are derived from cancer
CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides
CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that
CC is processed to at least one human leukocyte antigen (HLA) binding
CC peptide, which binds to Class I and Class II major histocompatibility
CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
CC but not normal colon, kidney, liver or brain tissue. The presence or
CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
CC cancer, especially testis tumours.

XX Sequence 9 AA;

Query Match 93.0%; Score 53; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQCF 10
| | | | | | | |
Db 1 lmwtqcf 9

RESULT 8

AAB69902

ID AAB69902 standard; Peptide; 9 AA.

AC AAB69902;

DT 27-APR-2001 (first entry)

DE Human NY-ESO-1 HLA binding motif #2.

XX
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.

OS Homo sapiens.

PN WO200107917-A1.

```

XX PD 01-FEB-2001.
XX PF 14-JUL-2000; 2000WO-US19220.
XX PR 23-JUL-1999; 99US-0359503.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX DR WPI; 2001-182822/18.
XX XX
XX Method useful for determining the status (e.g. progression, regression
XX or stability of the disease) of a cancerous condition, involves
XX determining the levels of NY-ESO-1 specific antibodies in a sample
XX taken from a patient -
XX
XX Example 14; Page 24; 50pp; English.
XX
XX The present sequence is given in a specification relating to a method
XX for determining the status of a cancerous condition in a patient
XX with a tumour that expresses NY-ESO-1. The method comprises assaying a
XX sample taken from the patient for antibodies that specifically bind to
XX the NY-ESO-1 and comparing the value obtained to a prior value obtained
XX from assay of a prior sample taken from the patient. Any difference
XX between the values is indicative of a change in status of the cancerous
XX condition. The method is useful for determining whether a cancerous
XX condition is progressing, regressing or remaining stable, in particular
XX in patients receiving treatment for a melanoma, adenocarcinoma,
XX non-small cell lung carcinoma or bladder carcinoma.
XX
XX Sequence 9 AA;
XX
XX Query Match 93.0%; Score 53; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 6.4e+05;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LLMWITQCF 9
XX | | | | |
XX Db 1 llmwitqcf 9
XX
XX RESULT 9
XX AAB69903
XX ID AAB69903 standard; Peptide; 9 AA.
XX AC AAB69903;
XX XX
XX DT 27-APR-2001 (first entry)
XX DE Human NY-ESO-1 HLA binding motif #3.
XX XX
XX KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
XX HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
XX non-small cell lung carcinoma; tumour status determination.
XX
XX OS Homo sapiens.
XX XX
XX PN WO200107917-A1.
XX XX
XX PD 01-FEB-2001.
XX XX
XX PF 14-JUL-2000; 2000WO-US19220.
XX XX
XX PR 23-JUL-1999; 99US-0359503.
XX XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX PA (CORR ) CORNELL RES FOUND INC.

```

```

XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX WPI; 2001-182822/18.
XX
XX Method useful for determining the status (e.g. progression, regression
XX or stability of the disease) of a cancerous condition, involves
XX determining the levels of NY-ESO-1 specific antibodies in a sample
XX taken from a patient -
XX
XX Example 14; Page 24; 50pp; English.
XX
XX The present sequence is given in a specification relating to a method
XX for determining the status of a cancerous condition in a patient
XX with a tumour that expresses NY-ESO-1. The method comprises assaying a
XX sample taken from the patient for antibodies that specifically bind to
XX the NY-ESO-1 and comparing the value obtained to a prior value obtained
XX from assay of a prior sample taken from the patient. Any difference
XX between the values is indicative of a change in status of the cancerous
XX condition. The method is useful for determining whether a cancerous
XX condition is progressing, regressing or remaining stable, in particular
XX in patients receiving treatment for a melanoma, adenocarcinoma,
XX non-small cell lung carcinoma or bladder carcinoma.
XX
XX Sequence 9 AA;
XX
XX Query Match 93.0%; Score 53; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 6.4e+05;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 LLMWITQCF 10
XX | | | | |
XX Db 1 llmwitqcf 9
XX
XX RESULT 10
XX AAY06006
XX ID AAY06006 standard; Peptide; 10 AA.
XX AC AAY06006;
XX XX
XX DT 16-AUG-1999 (first entry)
XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX XX
XX KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
XX leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
XX metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
XX uterine cancer; breast cancer; prostate cancer; ovarian cancer;
XX cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
XX liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
XX vaccine; human leukocyte antigen; HLA.
XX
XX OS Homo sapiens.
XX XX
XX PN WO9918206-A2.
XX XX
XX PD 15-APR-1999.
XX XX
XX PF 21-SEP-1998; 98WO-US19609.
XX XX
XX PR 08-OCT-1997; 97US-0061428.
XX XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX PI Rosenberg SA, Wang RP;
XX DR WPI; 1999-277270/23.
XX XX
XX PT Cancer antigen NY ESO1/CAG-3
XX PS Example 10; Page 42; 88pp; English.

```

XX This peptide was identified as an HLA peptide motif following a
 CC screen for epitopes from the coding region of human ESO-1/CAG-3
 CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
 CC The present peptide (ranked 19) corresponds to amino acid residues
 CC 157-166 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
 CC tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides (see AAY05967-87) derived from
 CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
 CC vaccines. A claimed method of preventing or inhibiting cancer
 CC involves administering a cancer peptide, with or without an HLA
 CC molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.

XX SQ Sequence 10 AA;

Query Match 93.0%; Score 53; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0097;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
 Db 2 llmwitqcf 10
 |||||

RESULT 11
 AAB85307
 ID AAB85307 standard; peptide; 10 AA.
 XX
 AC AAB85307;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE HLA-A2 binding NY-ESO-1 peptide (residues 157-166).
 KW NY-ESO-1; human leukocyte antigen; HLA; lysis; cytolytic T cell; CTL;
 KW HLA-A2; T-cell sorter; tumor; immune tetramer.
 XX
 OS Homo sapiens.
 XX
 PN WO200136453-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 08-NOV-2000; 2000WO-US42010.
 XX
 PR 15-NOV-1999; 99US-0440621.
 PR 25-FEB-2000; 2000US-0514036.
 PR 29-SEP-2000; 2000US-0676005.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYOX-) UNIV OXFORD.
 XX
 PI Valmori D, Cerottini J, Romero P, Cerundolo V;
 XX
 DR WPI; 2001-451454/48.
 XX
 XX Novel isolated NY-ESO-1 nonapeptide useful for determining if a cell
 PT presents human leukocyte antigen-A2 molecule on its surface, binds to
 PT human leukocyte antigen molecules and provokes lysis by cytolytic T
 PT cells -
 XX
 XX Example 11; Page 11; 38pp; English.
 PS
 CC The invention provides NY-ESO-1 peptide derivatives which bind to human
 CC leukocyte antigen (HLA) molecules and provokes lysis by cytolytic T cells
 CC (CTLs). The NY-ESO-1 nonapeptide is of formula SLLMWITQX, where X is an
 CC amino acid having an uncharged polar side chain. The NY-ESO-1 peptide

CC derivatives are useful for determining if a cell presents an HLA-A2
 CC molecule on its surface, by contacting a sample containing the cell with
 CC the peptide or its derivative, and determining binding between them,
 CC where the binding is indicative of HLA-A2 on the surface of the cell.
 CC The NY-ESO-1 peptides and analogues are useful therapeutically, for
 CC administration to a patient who is HLA-A2 positive and expresses NY-ESO-1
 CC in connection with the pathology, as well as diagnostically, i.e. to
 CC determine if HLA-A2 positive cells are present, or if relevant CTLs are
 CC present. They are also useful for determining the presence of CTLs in a
 CC sample. The peptides are useful as T-cell sorters, when incorporated into
 CC immune tetramers. The present sequence represents a NY-ESO-1 peptide
 CC that can bind to HLA-A2 molecule.

XX SQ Sequence 10 AA;

Query Match 93.0%; Score 53; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0097;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
 Db 2 llmwitqcf 10
 |||||

RESULT 12
 AAW62586
 ID AAW62586 standard; Peptide; 9 AA.
 XX
 AC AAW62586;
 XX
 DT 17-SEP-1998 (first entry)
 DE
 DE Cancer associated antigen peptide.
 XX
 XX Cancer associated antigen peptide.
 KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
 KW cancer; treatment; diagnosis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9814464-A1.
 XX
 PD 09-APR-1998.
 XX
 PF 15-SEP-1997; 97WO-US16335.
 XX
 PR 03-OCT-1996; 96US-0725182.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Chen Y, Drijfhout JW, Gure A, Jager E, Knuth A;
 PI Old LJ, Scanlan M;
 XX
 DR WPI; 1998-286417/25.
 XX
 PT New isolated cancer associated antigen - is used to develop products
 PT for the diagnosis and treatment of cancers and for monitoring cancer
 PT therapy
 XX
 PS Claim 33; Page 17; 49pp; English.
 XX
 CC Peptides AAW62585-87 are derived from cancer associated antigen
 CC NY-ESO-1, and are stimulators of cytotoxic T-cells. The specification
 CC describes a method for determining regression, progression of onset of a
 CC cancerous condition, comprising monitoring a sample from a patient
 CC with the cancerous condition for a parameter selected from NY-ESO-1
 CC protein, a peptide derived from NY-ESO-1 protein and cytolytic
 CC T cells specific for the peptide and an MHC molecule with which it
 CC non-covalently complexes. Methods for the treatment of a cancerous
 CC condition are also described. The NY-ESO-1 protein and peptides derived
 CC from it can be used for diagnosis and treatment of cancers and to
 CC monitor the efficacy of a therapeutic regime.

XX Sequence 9 AA;

Query Match 82.5%; Score 47; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
|||||
Db 2 llmwtqc 9

RESULT 13

AAAY01762
ID AAY01762 standard; Peptide; 9 AA.

XX AC AAY01762;

XX DT 25-JUN-1999 (first entry)

XX DE Exemplary antigenic peptide derived from NY-ESO-1.

XX KW MAGE-3; tumour associated gene; human leukocyte antigen Class II;
KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;
KW osteosarcoma; leukemia; carcinoma.

XX OS Homo sapiens.

XX PN W09914326-A1.

XX PD 25-MAR-1999.

XX PF 04-SEP-1998; 98WO-US18601.

XX PR 12-SEP-1997; 97US-0928615.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PA (UYVR-) UNIV VRIJE BRUSSEL.

XX PI Boon-Falleur T, Chau P, Corthals J, Heirman C;

XX PI Luiten R, Strobant V, Thielemans K, Van Der Bruggen P;

XX DR WPI; 1999-244031/20.

XX PT Isolated peptides that bind to human leukocyte antigen class II
molecules

XX PS Disclosure; Page 29; 88pp; English.

XX CC The present sequence represents an exemplary tumour associated peptide
antigen. The specification describes a MAGE-3 tumour associated gene.
XX CC Peptides (AAV01721-25) that bind human leukocyte antigen (HLA) class II
molecules can be derived from the MAGE-3 protein. These peptides and
XX CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide
and HLA Class II, are used to treat MAGE-3 related diseases,
XX CC particularly cancers (e.g. melanoma, osteosarcoma, leukemia and
XX CC various forms of carcinoma). The peptides are also used to produce
XX CC specific antibodies. Detection of the peptides, e.g. in binding
XX CC assays, particularly with antibodies, is used for diagnosis of such
XX CC diseases.

XX Sequence 9 AA;

Query Match 82.5%; Score 47; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
|||||
Db 2 llmwtqc 9

RESULT 14

AAAB08703
ID AAB08703 standard; Peptide; 9 AA.

XX AC AAB08703;

XX DT 02-JAN-2001 (first entry)

XX DE Antigenic peptide from tumour rejection antigen NY-ESO-1.

XX KW EphA3; HLA class II-binding peptide; human leukocyte antigen; antigen;
KW CD4+ T lymphocyte; tumour associated gene; vaccine.

XX OS Homo sapiens.

XX PN W0200050589-A1.

XX PD 31-AUG-2000.

XX PF 18-FEB-2000; 2000WO-US04326.

XX PR 22-FEB-1999; 99US-0121170.

XX PR 08-OCT-1999; 99US-0158566.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chiari R, Coulie P, Boon-Falleur T;

XX DR WPI; 2000-572089/53.

XX PT Novel tyrosine kinase receptor, EphA3 human leukocyte antigen (HLA)
class II binding peptide and nucleic acid encoding the receptor, useful
XX PT for diagnosing and treating conditions characterized by expression of
XX PT EphA3 gene

XX PS Disclosure; Page 36; 107pp; English.

XX CC AAB08668-B08704 represent antigenic peptides characteristic of tumours.
XX CC The peptides may be combined in vaccines with a human EphA3 HLA (human
XX CC leukocyte antigen) class II-binding peptide. EphA3 antigens, when
XX CC presented by an antigen presenting cell having a HLA class II molecule,
XX CC effectively induce activation and proliferation of CD4+ T lymphocytes.
XX CC EphA3 is a tumour associated gene. EphA3 HLA binding peptides are used
XX CC for selectively enriching a population of T lymphocytes. The peptides
XX CC are also used for diagnosing a disorder characterized by EphA3 or EphA3
XX CC HLA binding peptide expression. The peptides are also used to treat a
XX CC disorder characterized by EphA3 expression. The EphA3 binding peptides
XX CC are useful in producing vaccines and antibody.

XX Sequence 9 AA;

Query Match 82.5%; Score 47; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
|||||
Db 2 llmwtqc 9

RESULT 15

AAAB22791
ID AAB22791 standard; peptide; 9 AA.

XX AC AAB22791;

XX DT 22-DEC-2000 (first entry)

XX DE NY-ESO-1 peptide epitope, SEQ ID NO:2.

XX KW NY-ESO-1; epitope; CTL response; cytotoxic T lymphocyte; vaccine;

KW immunogenic; adjuvant coadministration; microbial infection;
KW tuberculosis; HIV; hepatitis B virus; hepatitis C virus; cancer.
XX Unidentified.
XX WO200048630-A1.
PN 24-AUG-2000.
PD 17-FEB-2000; 2000WO-AU00110.
XX 17-FEB-1999; 99AU-0008735.
PR 27-JUL-1999; 99AU-0001861.
XX (CSLC-) CSL LTD.
XX PA
XX PI Cox JC, Drane DP;
XX WPI; 2000-571930/53.
DR
XX Immunogenic complexes comprising negatively charged organic carrier
PT adjuvants and positively charged antigens for use as vaccines against
PT microbial infection and cancer
XX Example 4; Fig 5c; 11pp; English.
XX The invention relates to a novel immunogenic complex comprising a
CC charged organic carrier and a charged antigen which are
CC electrostatically associated. The complex induces a cytotoxic T
CC lymphocyte (CTL) response. The complex and/or vaccine can be used to
CC treat a disease in a mammal, where the complex/vaccine elicits, induces
CC or otherwise facilitates an immune response which inhibits, halts, delays
CC or prevents the onset or progression of the disease condition. In
CC particular, the disease is a condition resulting from a microbial
CC infection or cancer. Microbial infections which may be treated using the
CC immunogenic complex include human immunodeficiency virus (HIV), hepatitis
CC B, hepatitis C, tuberculosis or a parasitic condition, and cancers which
CC may be treated include melanoma, prostate cancer or breast cancer. The
CC complexes and vaccines simultaneously co-deliver antigen and adjuvant to
CC the same antigen presenting cell, which is often essential for induction
CC of appropriate immune responses. Sequences AAB22790-B22791 represent
CC peptide epitopes of the positively charged protein NY-ESO-1 used in an
CC exemplification of the invention.
XX
SQ Sequence 9 AA;

Query Match 82.5%; Score 47; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 llmwitqc 9
|||||||
llmwitqc 9

Search completed: July 16, 2002, 08:01:30
Job time: 783 sec

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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:00:52 ; Search time 73.89 Seconds
(without alignments)
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Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLWITQCFL 10

Scoring table: BLOSUM62
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Searched: 3502263 seqs, 351980561 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	57	100.0	10	19	US-09-529-206-92
3	57	100.0	10	19	US-09-529-206A-92
4	57	100.0	10	19	US-09-529-206B-92
5	53	93.0	9	18	US-09-409-455A-123
6	53	93.0	9	19	US-09-529-206-71
7	53	93.0	9	19	US-09-529-206-72

8	53	93.0	9	19	US-09-529-206A-71	Sequence 71, Appl
9	53	93.0	9	19	US-09-529-206A-72	Sequence 72, Appl
10	53	93.0	9	19	US-09-529-206B-71	Sequence 71, Appl
11	53	93.0	9	19	US-09-529-206B-72	Sequence 72, Appl
12	53	93.0	9	22	US-09-833-039-123	Sequence 123, Appl
13	53	93.0	10	19	US-09-529-206-95	Sequence 95, Appl
14	53	93.0	10	19	US-09-529-206A-95	Sequence 95, Appl
15	53	93.0	10	19	US-09-529-206B-95	Sequence 95, Appl
16	53	93.0	10	20	US-09-676-005B-11	Sequence 11, Appl
17	47	82.5	9	1	PCT-US00-04326-43	Sequence 43, Appl
18	47	82.5	9	2	PCT-US99-06875-5	Sequence 5, Appl
19	47	82.5	9	2	US-06-670-456A-1	Sequence 1, Appl
20	47	82.5	9	15	US-09-165-546A-5	Sequence 5, Appl
21	47	82.5	9	17	US-09-336-091-42	Sequence 42, Appl
22	47	82.5	9	17	US-09-396-315-80	Sequence 80, Appl
23	47	82.5	9	18	US-09-408-036B-5	Sequence 5, Appl
24	47	82.5	9	18	US-09-440-621-2	Sequence 2, Appl
25	47	82.5	9	19	US-09-510-635A-5	Sequence 5, Appl
26	47	82.5	9	19	US-09-574-749-34	Sequence 34, Appl
27	47	82.5	9	20	US-09-676-005B-2	Sequence 2, Appl
28	47	82.5	9	20	US-09-692-401-44	Sequence 44, Appl
29	47	82.5	9	20	US-09-697-884-80	Sequence 80, Appl
30	47	82.5	9	21	US-09-705-160-43	Sequence 43, Appl
31	47	82.5	9	21	US-09-751-798-5	Sequence 5, Appl
32	47	82.5	9	21	US-09-766-889A-51	Sequence 51, Appl
33	47	82.5	9	23	US-09-913-756-43	Sequence 43, Appl
34	47	82.5	9	24	US-10-023-182-5	Sequence 5, Appl
35	47	82.5	9	24	US-10-080-013-24	Sequence 24, Appl
36	47	82.5	9	26	US-60-336-968-12	Sequence 12, Appl
37	47	82.5	10	20	US-09-676-005B-13	Sequence 13, Appl
38	47	82.5	10	20	US-09-676-005B-14	Sequence 14, Appl
39	47	77.2	9	19	US-09-529-206-68	Sequence 68, Appl
40	44	77.2	9	19	US-09-529-206A-68	Sequence 68, Appl
41	44	77.2	9	19	US-09-529-206B-68	Sequence 68, Appl
42	44	77.2	10	19	US-09-529-206-94	Sequence 94, Appl
43	44	77.2	10	19	US-09-529-206A-94	Sequence 94, Appl
44	44	77.2	10	19	US-09-529-206B-94	Sequence 94, Appl
45	44	77.2	10	20	US-09-676-005B-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-09-165-546A-7
Sequence 7, Application US/09165546A
GENERAL INFORMATION:
APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gard
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CLASS II MOLECULES, AND USES THEREOF

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10158

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546A
FILING DATE: 02-Oct-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998

; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-165-546A-7

Query Match 100.0%; Score 57; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
DB 1 LLMWITQCFL 10

RESULT 2

; Sequence 92, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-92

Query Match 100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
DB 1 LLMWITQCFL 10

RESULT 3

; Sequence 92, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428

; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-92

Query Match 100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
DB 1 LLMWITQCFL 10

RESULT 4

; Sequence 92, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-92

Query Match 100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
DB 1 LLMWITQCFL 10

RESULT 5

; Sequence 123, Application US/09409455A
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Fireudschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622
; CURRENT APPLICATION NUMBER: US/09/409,455A
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-409-455A-123

Query Match 93.0%; Score 53; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCF 10
| | | | | | | |
Db 1 LLMWITQCF 9

RESULT 6
US-09-529-206-71
; Sequence 71, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-71

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCF 10
| | | | | | | |
Db 1 LLMWITQCF 9

RESULT 7
US-09-529-206-72
; Sequence 72, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-72

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
| | | | | | | |
Db 1 LLMWITQCF 9

RESULT 8
US-09-529-206A-71
; Sequence 71, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-71

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCF 10
| | | | | | | |
Db 1 LLMWITQCF 9

RESULT 9
US-09-529-206A-72
; Sequence 72, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-72

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
| | | | | | | |
Db 1 LLMWITQCF 9

RESULT 10
US-09-529-206B-71
; Sequence 71, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene

; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-71

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCF 10
Db 1 LLMWITQCF 9

RESULT 11
US-09-529-206B-72
; Sequence 72, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-72

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
Db 1 LLMWITQCF 9

RESULT 12
US-09-833-039-123
; Sequence 123, Application US/09833039
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040

; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039-123

Query Match 93.0%; Score 53; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCF 10
Db 1 LLMWITQCF 9

RESULT 13
US-09-529-206-95
; Sequence 95, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-95

Query Match 93.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
Db 2 LLMWITQCF 10

RESULT 14
US-09-529-206A-95
; Sequence 95, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-529-206A-95

Query Match 93.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
|||||
Db 2 LLMWITQCF 10

RESULT 15

US-09-529-206B-95
; Sequence 95, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-95

Query Match 93.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
|||||
Db 2 LLMWITQCF 10

Search completed: July 16, 2002, 08:04:54
Job time: 242 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:00:02 ; Search time 16.99 Seconds
(without alignments)
65.466 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 344541 seqs, 111227333 residues

Total number of hits satisfying chosen parameters: 37342

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	93.0	9	5 US-09-344-040C-123	Sequence 123, App
2	53	93.0	9	6 US-10-177-277-123	Sequence 123, App
3	47	82.5	9	1 PCT-US02-05748-24	Sequence 24, Appl
4	47	82.5	9	5 US-09-344-040C-131	Sequence 131, App
5	47	82.5	9	5 US-09-670-456A-1	Sequence 1, Appl
6	47	82.5	9	5 US-09-574-749B-34	Sequence 34, Appl
7	47	82.5	9	6 US-10-117-937-197	Sequence 197, App
8	47	82.5	9	6 US-10-177-277-131	Sequence 131, App
9	44	77.2	9	6 US-10-117-937-196	Sequence 196, App
10	38	66.7	9	1 PCT-US02-05748-25	Sequence 25, Appl
11	33	57.9	9	1 PCT-US02-05748-26	Sequence 26, Appl
12	33	57.9	9	5 US-09-344-040C-122	Sequence 122, App
13	33	57.9	9	5 US-09-344-040C-132	Sequence 132, App
14	33	57.9	9	5 US-09-574-749B-35	Sequence 35, Appl
15	33	57.9	9	6 US-10-177-277-122	Sequence 122, App
16	33	57.9	9	6 US-10-177-277-132	Sequence 132, App
17	33	57.9	10	5 US-09-344-040C-129	Sequence 129, App
18	33	57.9	10	6 US-10-117-937-203	Sequence 203, App
19	33	57.9	10	6 US-10-177-277-129	Sequence 129, App
20	30	52.6	9	5 US-09-595-334C-638	Sequence 638, App
21	30	52.6	9	5 US-09-602-016C-638	Sequence 638, App
22	30	52.6	9	5 US-09-570-582C-797	Sequence 797, App
23	30	52.6	9	5 US-09-602-152C-638	Sequence 638, App
24	30	52.6	9	5 US-09-621-630B-638	Sequence 638, App
25	30	52.6	10	6 US-10-103-299-3789	Sequence 3789, App
26	29	50.9	9	6 US-10-117-937-202	Sequence 202, App

27	49.1	9	6	US-10-117-937-199	Sequence 199, App
28	47.4	7	6	US-10-083-894-9	Sequence 9, Appl
29	40.4	8	5	US-09-722-250-259	Sequence 259, App
30	40.4	8	5	US-09-722-250-259	Sequence 259, App
31	40.4	9	5	US-09-722-250-374	Sequence 374, App
32	40.4	9	5	US-09-722-250-374	Sequence 374, App
33	40.4	4	5	US-09-573-655B-2844	Sequence 2844, App
34	38.6	4	5	US-09-692-714A-349	Sequence 349, App
35	38.6	4	5	US-09-692-717A-349	Sequence 349, App
36	38.6	4	5	US-09-620-393B-9512	Sequence 9512, App
37	38.6	4	5	US-09-696-751-349	Sequence 32674, A
38	38.6	4	5	US-09-935-625-32674	Sequence 32674, A
39	38.6	7	5	US-09-722-250-287	Sequence 287, App
40	38.6	7	5	US-09-722-250-287	Sequence 287, App
41	38.6	8	5	US-09-595-334C-459	Sequence 459, App
42	38.6	8	5	US-09-602-016C-459	Sequence 459, App
43	38.6	8	5	US-09-573-655B-3020	Sequence 3020, App
44	38.6	8	5	US-09-587-811A-5	Sequence 5, Appl
45	38.6	8	5	US-09-570-582C-618	Sequence 618, App

ALIGNMENTS

RESULT 1
US-09-344-040C-123
; Sequence 123, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-123

Query Match 93.0%; Score 53; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLWITQCFL 10
 | |
Db 1 LLWITQCFL 9

RESULT 2
US-10-177-277-123
; Sequence 123, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1

; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-123

Query Match 93.0%; Score 53; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCFL 10
 |||||
Db 1 LLMWITQCFL 9

RESULT 3
PCT-US02-05748-24
; Sequence 24, Application PC/TUS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-05748-24

Query Match 82.5%; Score 47; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
 |||||
Db 2 LLMWITQC 9

RESULT 4
US-09-344-040C-131
; Sequence 131, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Expression of an SXX Gene, Peptides Derived From Said SXX Gene and Uses Thereof
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5356.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839

; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-131

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
 |||||
Db 2 LLMWITQC 9

RESULT 5
US-09-670-456A-1
; Sequence 1, Application US/09670456A
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjatich, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-456A-1

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
 |||||
Db 2 LLMWITQC 9

RESULT 6
US-09-574-749B-34
; Sequence 34, Application US/09574749B
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL DEVICES
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 9

;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-34

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 7
US-10-117-937-197
; Sequence 197, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-197

Query Match 82.5%; Score 47; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 8
US-10-177-277-131
; Sequence 131, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining Expression of an Ssx Gene, Peptides Derived From Said Ssx Gene and Uses Thereof
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130

;
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-131

Query Match 82.5%; Score 47; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 9
US-10-117-937-196
; Sequence 196, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-196

Query Match 77.2%; Score 44; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 WITQCFL 10
| | | | | | | |
Db 1 WITQCFL 7

RESULT 10
PCT-US02-05748-25
; Sequence 25, Application PC/TUS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-05748-25

Query Match 66.7%; Score 38; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQ 7
Db 2 LLMWITQ 8

RESULT 11
PCT-US02-05748-26
; Sequence 26, Application PC/TUS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-05748-26

Query Match 57.9%; Score 33; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWIT 6
Db 4 LLMWIT 9

RESULT 12
US-09-344-040C-122
; Sequence 122, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschtuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 122
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-122

Query Match 57.9%; Score 33; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWIT 6
Db 4 LLMWIT 9

RESULT 13
US-09-344-040C-132
; Sequence 132, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschtuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-132

Query Match 57.9%; Score 33; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWIT 6
Db 4 LLMWIT 9

RESULT 14
US-09-574-749B-35
; Sequence 35, Application US/09574749B
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source

US-09-574-749B-35

Query Match 57.9%; Score 33; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWIT 6
Db 4 LLMWIT 9

RESULT 15

US-10-177-277-122
; Sequence 122, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 122
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-122

Query Match 57.9%; Score 33; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWIT 6
Db 4 LLMWIT 9

Search completed: July 16, 2002, 08:03:20
Job time: 198 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:56:42 ; Search time 15.68 Seconds
(without alignments)
15.578 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFLL 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 70601

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	4 US-09-359-503-7	Sequence 7, Appli
2	47	82.5	9	4 US-09-183-931-43	Sequence 43, Appl
3	47	82.5	9	4 US-09-359-503-5	Sequence 5, Appli
4	47	82.5	9	4 US-09-062-422-5	Sequence 5, Appli
5	47	82.5	9	4 US-09-937-263B-5	Sequence 5, Appli
6	47	82.5	9	4 US-09-166-448-80	Sequence 80, Appl
7	33	57.9	6	4 US-09-359-503-14	Sequence 14, Appl
8	33	57.9	6	4 US-09-062-422-7	Sequence 7, Appli
9	33	57.9	6	4 US-09-937-263B-7	Sequence 7, Appli
10	33	57.9	9	4 US-09-183-931-44	Sequence 44, Appl
11	33	57.9	9	4 US-09-359-503-6	Sequence 6, Appli
12	33	57.9	9	4 US-09-062-422-6	Sequence 6, Appli
13	33	57.9	9	4 US-09-937-263B-6	Sequence 6, Appli
14	33	57.9	9	4 US-09-166-448-81	Sequence 81, Appl
15	27	47.4	8	4 US-09-020-065A-24	Sequence 24, Appl
16	26	45.6	6	2 US-08-482-228-186	Sequence 186, App
17	26	45.6	6	3 US-08-482-528-186	Sequence 186, App
18	26	45.6	10	4 US-09-248-588-35	Sequence 35, Appl
19	25	43.9	9	1 US-08-484-044-7	Sequence 7, Appli
20	25	43.9	10	3 US-08-768-859A-15	Sequence 15, Appl
21	25	43.9	10	3 US-08-767-820A-15	Sequence 15, Appl
22	25	43.9	10	5 PCT-US95-06157-15	Sequence 15, Appl
23	24	42.1	10	4 US-08-379-580-6	Sequence 6, Appli
24	23	40.4	6	1 US-07-620-426B-2	Sequence 2, Appli
25	23	40.4	6	1 US-07-662-007B-2	Sequence 2, Appli
26	23	40.4	6	1 US-07-624-247-2	Sequence 2, Appli
27	23	40.4	6	3 US-08-470-204A-2	Sequence 2, Appli

28 23 40.4 8 4 US-09-258-754-259 Sequence 259, App
29 23 40.4 8 4 US-09-042-107-259 Sequence 259, App
30 23 40.4 9 4 US-09-258-754-374 Sequence 374, App
31 23 40.4 9 4 US-09-042-107-374 Sequence 374, App
32 23 40.4 10 2 US-08-764-640-103 Sequence 103, App
33 23 40.4 10 3 US-08-159-339A-477 Sequence 477, App
34 23 40.4 10 3 US-08-973-225-103 Sequence 103, App
35 23 40.4 10 3 US-09-244-298A-103 Sequence 103, App
36 23 40.4 10 4 US-08-378-313-11 Sequence 11, Appl
37 23 40.4 10 4 US-09-516-704-103 Sequence 103, App
38 22 38.6 6 2 US-08-621-803-182 Sequence 182, App
39 22 38.6 6 2 US-08-621-803-183 Sequence 183, App
40 22 38.6 6 2 US-08-621-259A-149 Sequence 149, App
41 22 38.6 6 4 US-09-217-352-182 Sequence 182, App
42 22 38.6 6 4 US-09-217-352-183 Sequence 183, App
43 22 38.6 6 4 US-09-344-541A-59 Sequence 59, Appl
44 22 38.6 6 5 PCT-US95-09262-149 Sequence 149, App
45 22 38.6 7 1 US-08-064-517-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-7
; Sequence 7, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

to

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;
; TOPOLOGY: linear
; US-09-359-503-7

Query Match      100.0%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCEL 10
Db 1 LLMWITQCEL 10

RESULT 2
US-09-183-931-43
; Sequence 43, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; FILE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527.1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018,422
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
; US-09-183-931-43

Query Match      82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 3
US-09-359-503-5
; Sequence 5, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; FILE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999

Query Match      82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 4
US-09-062-422-5
; Sequence 5, Application us/09062422
; Patent No. 6252052
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tsung; Scanlan, Matthew; Knuth, Alexander;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
; FILE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,422
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
```

NAME: Hanson, No. 6252052man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-062-422-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 5
US-08-937-263B-5
Sequence 5, Application US/08937263B
Patent No. 6274145
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tsang; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Simm, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-937-263B-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8

Db 2 LLMWITQC 9

RESULT 6
US-09-166-448-80
Sequence 80, Application US/09166448
Patent No. 6291430
GENERAL INFORMATION:
APPLICANT: Chau, Pascal
APPLICANT: Vantobant, Valrie
APPLICANT: Stroobant, Vincent
APPLICANT: Boon-Palleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Thielemans, Kris
APPLICANT: Corthals, Jorgen
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
FILE REFERENCE: L0461/7052
CURRENT APPLICATION NUMBER: US/09/166,448
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 80
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-166-448-80

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 7
US-09-359-503-14
Sequence 14, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263

```
/ FILING DATE: September 15, 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/752,182
/ FILING DATE: 03-October-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, No. 6251603man D.
/ REGISTRATION NUMBER: 30,946
/ REFERENCE/DOCKET NUMBER: LUD 5466.1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 318-3000
/ TELEFAX: (212) 752-5958
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-09-359-503-14

Query Match 57.9%; Score 33; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
Db 1 LLMWIT 6

RESULT 8
US-09-062-422-7
; Sequence 7, Application US/09062422
; Patent No. 6252052
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
; NUMBER OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,422
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6252052man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
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/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-09-062-422-7

Query Match 57.9%; Score 33; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
Db 1 LLMWIT 6

RESULT 9
US-08-937-263B-7
; Sequence 7, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-937-263B-7

Query Match 57.9%; Score 33; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
Db 1 LLMWIT 6

RESULT 10
US-09-183-931-44
; Sequence 44, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
```


APPLICANT: Van Baren, Nicolas
APPLICANT: Brasseur, Francis
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
FILE REFERENCE: LUD 5527.1-JEL/ES
CURRENT APPLICATION NUMBER: US/09/183,931C
CURRENT FILING DATE: 2000-02-28
EARLIER APPLICATION NUMBER: US 09/018,422
EARLIER FILING DATE: 1998 - 02 - 04
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 44
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION:
US-09-183-931-44

Query Match 57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
Db 4 LLMWIT 9

RESULT 11
US-09-359-503-6
Sequence 6, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-359-503-6

Query Match 57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
Db 4 LLMWIT 9

RESULT 12
US-09-062-422-6
Sequence 6, Application US/09062422
Patent No. 6252052
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
TITLE OF INVENTION: THEREFROM
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,422
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6252052man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-062-422-6

Query Match 57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
| | | | |
Db 4 LLMWIT 9

RESULT 13
US-08-937-263B-6
; Sequence 6, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-6

Query Match 57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
| | | | |
Db 4 LLMWIT 9

RESULT 14
US-09-166-448-81
; Sequence 81, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052

Query Match 47.4%; Score 27; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LWMITOC 8
| : | | |
Db 2 LQYLTOC 8

; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-81

Query Match 57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
| | | | |
Db 4 LLMWIT 9

RESULT 15
US-09-020-065A-24
; Sequence 24, Application US/09020065A
; Patent No. 6346602
; GENERAL INFORMATION:
; APPLICANT: Townsend, Robert M.
; APPLICANT: Korngold, Robert
; TITLE OF INVENTION: Peptide Mimics of the Cytokine Receptor Common
; TITLE OF INVENTION: Gamma Chain and Methods and Compositions for
; TITLE OF INVENTION: Making and Using the Same
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6346602 is LLP
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Wordperfect V. 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,065A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,941
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-2291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-020-065A-24

Query Match 47.4%; Score 27; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LWMITOC 8
| : | | |
Db 2 LQYLTOC 8

Search completed: July 16, 2002, 08:02:06
Job time: 324 sec